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Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 2
AX003761
LOCUS       AX003761                321 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 55 from Patent WO9925818.
ACCESSION   AX003761
VERSION     AX003761.1  GI:9927567
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Method of identifying binding site domains that retain the capacity
            of binding to an epitope
  JOURNAL   Patent: WO 9925818-A 55 27-MAY-1999;
            KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.5%;  Score 316.2;  DB 6;  Length 321;
  Best Local Similarity   99.1%;  Pred. No. 3.7e-91;
  Matches  318;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 3
BD075293
LOCUS       BD075293                321 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel method for the production of anti-human antigen receptors and
            uses thereof.
ACCESSION   BD075293
VERSION     BD075293.1  GI:22620896
KEYWORDS    JP 2001519824-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Novel method for the production of anti-human antigen receptors and
            uses thereof
  JOURNAL   Patent: JP 2001519824-A 22 23-OCT-2001;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001519824-A/22
            PD   23-OCT-2001
            PF   14-APR-1998 JP 1998543494
            PR   14-APR-1997 EP   97106109.8
            PI   PETER KUFER,TOBIAS RAUM
            PC   C07K16/00,C07K16/30,A61K39/395
            CC   Novel method for the production of anti-human antigen  CC
                  receptors and uses
            CC   thereof
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(321).
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             98.5%;  Score 316.2;  DB 6;  Length 321;
  Best Local Similarity   99.1%;  Pred. No. 3.7e-91;
  Matches  318;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 4
BD139668
LOCUS       BD139668                321 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  A novel method of identifying binding site domains that retain the
            capacity of binding to an epitope.
ACCESSION   BD139668
VERSION     BD139668.1  GI:23234613
KEYWORDS    JP 2002508924-A/53.
SOURCE      Homo sapiens (human)
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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P., Raum,T., Borschert,K., Zettl,F. and Lutterbuese,R.
  TITLE     A novel method of identifying binding site domains that retain the
            capacity of binding to an epitope
  JOURNAL   Patent: JP 2002508924-A 53 26-MAR-2002;
            PETER KUFER
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508924-A/53
            PD   26-MAR-2002
            PF   16-NOV-1998 JP 2000521184
            PR   17-NOV-1997 EP   97120096.9
            PI   PETER KUFER,TOBIAS RAUM,KATRIN BORSCHERT,FLORIAN ZETTL,RALF
            PI   LUTTERBUESE
            PC   C12N15/09,A61K38/00,A61K38/22,A61K38/43,A61K39/395,C07K14/705,
            PC   C07K16/30,
            PC   C12N1/21,C12N5/10,C12P21/02,C12P21/08,G01N33/566,C12N15/00, PC
              A61K37/02,
            PC   A61K37/24,A61K37/48,C12N5/00
            CC   A novel method of identifying binding site
            domains that retain
            CC             the
            CC   capacity of binding to an epitope
            FH   Key             Location/Qualifiers
            FT   source          1. .321
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .321
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             98.5%;  Score 316.2;  DB 6;  Length 321;
  Best Local Similarity   99.1%;  Pred. No. 3.7e-91;
  Matches  318;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 5
A84380
LOCUS       A84380                   321 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 147 from Patent WO9846645.
ACCESSION   A84380
VERSION     A84380.1  GI:6733303
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
            USES THEREOF
  JOURNAL   Patent: WO 9846645-A 147 22-OCT-1998;
            KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES              Location/Qualifiers
     source           1. .321
                      /organism="unidentified"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:32644"
     CDS              <1. .>321
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAB69290.1"
                      /db_xref="GI:6733304"
                      /translation="ELQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGQPP
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                      RLDIQ"
ORIGIN

  Query Match             79.6%;  Score 255.4;  DB 6;  Length 321;
  Best Local Similarity   87.2%;  Pred. No. 2e-71;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  |||||||||| ||| ||||||||||||||||||| || || |||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| ||||||| ||||| ||| | ||    | |||  ||| || |||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        301 GGGACACGACTGGACATTCAA 321


RESULT 6
BD075296
LOCUS       BD075296                 321 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel method for the production of anti-human antigen receptors and
            uses thereof.
ACCESSION   BD075296
VERSION     BD075296.1  GI:22620899
KEYWORDS    JP 2001519824-A/25.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Novel method for the production of anti-human antigen receptors and
            uses thereof
  JOURNAL   Patent: JP 2001519824-A 25 23-OCT-2001;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001519824-A/25
            PD   23-OCT-2001
            PF   14-APR-1998 JP 1998543494
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            PR   14-APR-1997 EP   97106109.8
            PI   PETER KUFER,TOBIAS RAUM
            PC   C07K16/00,C07K16/30,A61K39/395
            CC   Novel method for the production of anti-human antigen  CC
                 receptors and uses
            CC   thereof
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(321).
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           79.6%;  Score 255.4;  DB 6;  Length 321;
  Best Local Similarity   87.2%;  Pred. No. 2e-71;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  |||||||||| ||| |||||||||||||||||| || || |||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        301 GGGACACGACTGGACATTCAA 321


RESULT 7
BD222938
LOCUS       BD222938               1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222938
VERSION     BD222938.1  GI:33032708
KEYWORDS    JP 2002521053-A/32.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 32 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/32
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC   (C12N5/00,C12R1:91)
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            FH   Key             Location/Qualifiers
            FT   CDS             (39). .(1607).
FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           79.6%;  Score 255.4;  DB 6;  Length 1630;
  Best Local Similarity   87.2%;  Pred. No. 2.1e-71;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  |||||||||| ||| |||||||||||||||||| || || |||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 8
BD222939
LOCUS       BD222939               1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222939
VERSION     BD222939.1  GI:33032709
KEYWORDS    JP 2002521053-A/33.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 33 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/33
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC   (C12N5/00,C12R1:91)
            CC   Heterominibodies
            FH   Key             Location/Qualifiers
            FT   CDS             (39). .(1610).
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FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             79.6%;  Score 255.4;  DB 6;  Length 1630;
  Best Local Similarity   87.2%;  Pred. No. 2.1e-71;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  ||||||||| ||| ||||||||||||||||| || || |||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| |||||||  ||||| |||  | ||   | |||  ||| || |||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 9
AX023365
LOCUS       AX023365               1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 36 from Patent WO0006605.
ACCESSION   AX023365
VERSION     AX023365.1  GI:10183777
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 36 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             39. .1610
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC08835.1"
                     /db_xref="GI:10183778"
                     /translation="MGWSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
                     SQSISSYLNWYQQKPGQPPKLLIYWASTRESGVPDRFSGSESGTNYTLTISSLQPEDF
                     ATYFCQQSDSLPITFGQGTRLDIQGGGGSGGGGSGGGGSEVQLLESGGGVVQPGRSLR
                     LSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN
                     TLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTTVTVSSGTPLGDTT
                     HTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                     LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTSGGGGSAP
                     ARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                     LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIP
                     FDCWEPVQEHHHHHH"
ORIGIN

  Query Match             79.6%;  Score 255.4;  DB 6;  Length 1630;
  Best Local Similarity   87.2%;  Pred. No. 2.1e-71;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  ||||||||| ||| ||||||||||||||||| || || |||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| |||||||  ||||| |||  | ||   | |||  ||| || |||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 10
AX023367
LOCUS       AX023367               1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 38 from Patent WO0006605.
ACCESSION   AX023367
VERSION     AX023367.1  GI:10183779
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 38 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
FEATURES             Location/Qualifiers
     source          1. .1630
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             39. .1613
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC08836.1"
                     /db_xref="GI:10183780"
                     /translation="MGWSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
                     SQSISSYLNWYQQKPGQPPKLLIYWASTRESGVPDRFSGSESGTNYTLTISSLQPEDF
                     ATYFCQQSDSLPITFGQGTRLDIQGGGGSGGGGSGGGGSEVQLLESGGGVVQPGRSLR
                     LSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN
                     TLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTTVTVSSGTPLGDTT
                     HTRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
                     TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGSA
                     PTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL
                     EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF
                     LNRWITFCQSIISTLT"
ORIGIN

  Query Match             79.6%;  Score 255.4;  DB 6;  Length 1630;
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  Best Local Similarity   87.2%;  Pred. No. 2.1e-71;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||| ||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  |||||||||| ||| ||||||||||||||||||| || ||| |
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| |||||||  ||||| ||| | ||    | |||  ||| || |||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 11
AB063929
LOCUS       AB063929                324 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
            region, partial cds, clone:K102.
ACCESSION   AB063929
VERSION     AB063929.1  GI:21669064
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 324)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="K102"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
     gene            1. .324
                     /gene="IGK"
     CDS             <1. .>324
                     /gene="IGK"
                     /codon_start=1
                     /product="immunoglobulin kappa light chain VLJ region"
                     /protein_id="BAC01557.1"
                     /db_xref="GI:21669065"
                     /translation="DIQMTQSPSSLSASVGDRVTITCRASQSISSYLNWYQQKPGKAP
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                     KLEIKR"
ORIGIN

  Query Match             77.6%;  Score 249;  DB 9;  Length 324;
  Best Local Similarity   86.0%;  Pred. No. 2.3e-69;
  Matches  276;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||      ||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| |||||||||    | ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              ||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 12
AB064098
LOCUS       AB064098                828 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
            region, partial cds, clone:K57.
ACCESSION   AB064098
VERSION     AB064098.1  GI:21669402
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 828)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1. .828
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="K57"
                     /clone_lib="AIMS4"
                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
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                     /gene="IGK"
     CDS             1. .>828
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                     /protein_id="BAC01726.1"
                     /db_xref="GI:21669403"
                     /translation="MKYLLPTAAAGLLLLAAQPAMADIQMTQSPSSLSASVGDRVTIT
                     CRASQSISSYLNWYQQKPGKAPKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQP
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                     FYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTLTLSKADYEKHKVYACEV
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                     "
     sig_peptide     1. .66
                     /gene="IGK"
                     /note="pelB signal peptide"
ORIGIN

  Query Match             77.6%;  Score 249;  DB 9;  Length 828;
  Best Local Similarity   86.0%;  Pred. No. 2.4e-69;
  Matches  276;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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Db        127 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 186

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 306

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| |||||||||   | ||||||||||||||||||||
Db        307 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAG 366

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        367 GGGACCAAGCTGGAGATCAAA 387


RESULT 13
E12913
LOCUS       E12913                   321 bp    DNA     linear   PAT 27-APR-1998
DEFINITION  Human cDNA encoding variable region of light chain anti-pulmonary
            carcinoma monoclonal antibody.
ACCESSION   E12913
VERSION     E12913.1  GI:3251744
KEYWORDS    JP 1997098786-A/2.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Shirahata,S., Mochizuki,K. and Kato,M.
  TITLE     ANTIBODY CDNA
  JOURNAL   Patent: JP 1997098786-A 2 15-APR-1997;
            MORINAGA & CO LTD, RES DEV CORP OF JAPAN
COMMENT     OS   Homo sapiens (human)
            PN   JP 1997098786-A/2
            PD   15-APR-1997
            PF   06-OCT-1995 JP 1995284400
            PI   SHIRAHATA SANETAKA, MOCHIZUKI KATSUMI, KATO MASATOSHI PC
            C12N15/09,C07H21/04,C07K16/32,C12P21/08//C12N5/10,(C12P21/08, PC
            C12R1:91),
            PC   (C12N5/10,C12R1:91);
            CC   strandedness: Double;
            CC   topology: Linear;
            FH   Key             Location/Qualifiers
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            FT   source          1. .321
            FT                   /organism='Homo sapiens'
            FT                   /cell_type='hybridoma cell'
            FT                   /cell_line='AE-6'
            FT   mat_peptide     1. .321
            FT                   /product='variable region of light chain  FT
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            FT                   carcinoma monoclonal antibody' FT
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            FT   misc_feature    148. .168
            FT                   /note='this region encodes Complementarity  FT
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            FT                   region (CDR-2)'
            FT   misc_feature    265. .291
            FT                   /note='this region encodes Complementarity  FT
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            FT                   region (CDR-3)'.
FEATURES             Location/Qualifiers
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                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             76.6%;  Score 245.8;  DB 6;  Length 321;
  Best Local Similarity   85.4%;  Pred. No. 2.6e-68;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCCGTCTGCATCTGTCGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||| ||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCACCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||| || || ||       ||| |     | || | ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAACTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
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Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACAGTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 14
HUMIGKC
LOCUS       HUMIGKC                  324 bp    mRNA    linear   PRI 27-JUL-1994
DEFINITION  Human IgK (thyroid peroxidase-specific Fab fragment) mRNA, partial
            cds.
ACCESSION   L12108
VERSION     L12108.1  GI:397789
KEYWORDS    V-region; autoimmune; immunoglobulin kappa-chain.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
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  AUTHORS   Portolano,S., McLachlan,S.M. and Rapoport,B.
  TITLE     High affinity, thyroid-specific human autoantibodies displayed on
            the surface of filamentous phage use V genes similar to other
            autoantibodies
  JOURNAL   J. Immunol. 151 (5), 2839-2851 (1993)
  MEDLINE   93367244
   PUBMED   8360495
COMMENT     Original source text: Homo sapiens cDNA to mRNA.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /map="2p12"
     gene            1. .324
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                     /db_xref="GI:397790"
                     /translation="ELVMTQSPSSLSASVGDRVIITCRASQSISSYLNWYQQKPGTAP
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                     KLEIKR"
ORIGIN

  Query Match             76.6%;  Score 245.8;  DB 9;  Length 324;
  Best Local Similarity   85.4%;  Pred. No. 2.6e-68;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db          1 GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCATT 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||      | ||||| || || || ||       ||| ||    | ||   ||||||||
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Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
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Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACGGGACCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 15
AB063952
LOCUS       AB063952                321 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGK mRNA for immunoglobulin kappa light chain VLJ
            region, partial cds, clone:K125.
ACCESSION   AB063952
VERSION     AB063952.1  GI:21669110
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 321)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1. .321
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                     /db_xref="taxon:9606"
                     /clone="K125"
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                     /note="mixture of tissues:tonsils, umbilical cords,
                     peripheral blood and bone marrow"
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     CDS             <1. .>321
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                     KLEIK"
ORIGIN

  Query Match             76.1%;  Score 244.2;  DB 9;  Length 321;
  Best Local Similarity   85.0%;  Pred. No. 8.5e-68;
  Matches  273;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCGTCTATAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||| |||| |||||||||||| || ||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGTTATTTAAATTGGTATCAACACAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||| ||||| || ||       ||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAACTGCTGATCTATGCTGCATCCAATTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| ||||||||| | | ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAATACCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


Search completed: December  7, 2004, 08:53:00
Job time : 1817.78 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 22:52:33 ; Search time 271.757 Seconds
(without alignments)
6200.629 Million cell updates/sec

Title: US-09-403-107-141
Perfect score: 321
Sequence: 1 gagctccagatgacccagtc.....ggaccaagctggagatcaaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
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2: geneseqn1990s:*
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4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	316.2	98.5	321	2	AAV68536	Aav68536 Nucleotid
2	316.2	98.5	321	2	AAX77237	Aax77237 Human kap
3	255.4	79.6	321	2	AAV68539	Aav68539 Nucleotid
4	255.4	79.6	1630	3	AAZ50588	Aaz50588 HD70scFv-
5	255.4	79.6	1630	3	AAZ50587	Aaz50587 HD70scFv-
6	245.8	76.6	321	2	AAT66781	Aat66781 Anti-canc
7	242.6	75.6	333	5	AAH74685	Aah74685 Nucleotid
8	242.6	75.6	333	10	ABT34321	Abt34321 Hepatitis
9	242.6	75.6	720	10	ABT34316	Abt34316 Hepatitis
10	242.6	75.6	900	5	AAH74689	Aah74689 Nucleotid
11	242.6	75.6	900	10	ABT34325	Abt34325 Hepatitis
12	239.2	74.5	321	5	AAH68701	Aah68701 Human ant
13	239.2	74.5	321	9	ACD45365	Acd45365 Anti-Rh(D
14	237.8	74.1	333	5	AAH74684	Aah74684 Nucleotid
15	237.8	74.1	333	10	ABT34320	Abt34320 Hepatitis
16	237.8	74.1	720	10	ABT34315	Abt34315 Hepatitis
17	237.8	74.1	900	5	AAH74688	Aah74688 Nucleotid
18	237.8	74.1	900	10	ABT34324	Abt34324 Hepatitis
19	236.2	73.6	324	10	AAL52120	Aal52120 Human ant
20	236.2	73.6	396	2	AAT75423	Aat75423 Human ant
21	236.2	73.6	720	2	AAX36070	Aax36070 DNA encod
22	236.2	73.6	720	10	ABZ76706	Abz76706 Human ser
23	236.2	73.6	720	12	ADL92368	Adl92368 Human pha
24	236	73.5	321	5	AAH68658	Aah68658 Human ant
25	236	73.5	321	9	ACD45322	Acd45322 Anti-Rh(D
26	234.6	73.1	315	2	AAV19765	Aav19765 Antibody
27	234.6	73.1	322	6	ABS62720	Abs62720 Anti-IGF-
28	234.6	73.1	729	3	AAA11630	Aaa11630 Human imm
29	234.6	73.1	729	6	ABL46009	Abl46009 Humanised
30	233	72.6	315	2	AAV19767	Aav19767 Antibody
31	231.4	72.1	321	12	ADL93583	Adl93583 Human CD4
32	231.4	72.1	321	12	ADO06842	Ado06842 Virucidal
33	231.4	72.1	324	4	AAF29073	Aaf29073 Human HIV
34	231.4	72.1	324	10	AAL52122	Aal52122 Human ant
35	231.4	72.1	1106	6	ABQ54241	Abq54241 Human ova
36	231.2	72.0	321	5	AAH68654	Aah68654 Human ant
37	231.2	72.0	321	9	ACD45318	Acd45318 Anti-Rh(D
38	230	71.7	341	2	AAT60119	Aat60119 Coding se
39	229.8	71.6	315	2	AAV19761	Aav19761 Antibody
40	229.8	71.6	324	12	ADL92385	Adl92385 Anti-HSA
41	229.8	71.6	333	2	AAX79686	Aax79686 Human can
42	229.8	71.6	342	4	AAH47727	Aah47727 Nucleotid
43	229.6	71.5	321	5	AAH68720	Aah68720 Human ant
44	229.6	71.5	321	5	AAH68647	Aah68647 Human ant
45	229.6	71.5	321	9	ACD45311	Acd45311 Anti-Rh(D

ALIGNMENTS

RESULT 1
AAV68536
ID AAV68536 standard; DNA; 321 BP.
XX
AC AAV68536;
XX
DT 16-FEB-1999 (first entry)
XX
DE Nucleotide sequence of human Kappa 8 light chain variable region.
XX
KW Human; kappa 8 light chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .321
FT /*tag= a
FT /product= "human kappa 8 light chain variable region"
XX
PN WO9846645-A2.
XX
PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-EP002180.
XX
PR 14-APR-1997; 97EP-00106109.
XX
PA (KUFE/) KUFER P.
PA (RAUM/) RAUM T.
XX
PI Kufer P, Raum T;
XX
DR WPI; 1998-594564/50.
DR P-PSDB; AAW80814.
XX
PT Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.
XX
PS Claim 9; Fig 6; 84pp; English.
XX
CC This is the nucleotide sequence of the human kappa 8 light chain variable

```
CC   region, used in the method of the invention. for providing receptors that
CC   can be used for targeting antigens in humans without being immunogenic
CC   themselves. Such receptors can be used for treating diseases such as
CC   tumours or auto-immune diseases, graft rejection after transplantation,
CC   infectious diseases by targeting cellular receptors as well as allergic,
CC   inflammatory, endocrine and degenerative diseases by targeting key
CC   molecules involved in the pathological process
XX
SQ   Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;

  Query Match             98.5%;  Score 316.2;  DB 2;  Length 321;
  Best Local Similarity   99.1%;  Pred. No. 2.9e-93;
  Matches  318;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 2
AAX77237
ID   AAX77237 standard; DNA; 321 BP.
XX
AC   AAX77237;
XX
DT   04-AUG-1999  (first entry)
XX
DE   Human kappa 8 light chain variable region encoding DNA.
XX
KW   Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW   autoimmune disease; scFv-antibody; single-chain Fv; ss.
XX
OS   Homo sapiens.
XX
PN   WO9925818-A1.
XX
PD   27-MAY-1999.
XX
PF   16-NOV-1998;   98WO-EP007313.
XX
PR   17-NOV-1997;   97EP-00120096.
XX
PA   (KUFE/) KUFER P.
XX
PI   Kufer P,  Raum T,  Borschert K,  Zettl F,  Lutterbuese R;
XX
DR   WPI; 1999-338004/28.
DR   P-PSDB; AAY17955.
XX
PT   Phage display system for identification of binding site domains retaining
PT   capacity to bind an epitope.
XX
PS   Disclosure; Fig 3.2; 152pp; English.
XX
CC   The invention relates to a method of identifying binding site domains
CC   (BSD) that retain the capacity of binding to a predetermined epitope when
CC   positioned C-terminal of at least one further domain in a recombinant bi-
CC   or multivalent polypeptide. The method comprises (a) testing a panel of
CC   BSD displayed on the surface of a biological display system as part of a
CC   fusion protein for binding to a predetermined epitope, where the fusion
CC   protein comprises an additional domain positioned N-terminal of the BSD
CC   and an amino acid sequence that mediates anchoring of the fusion protein
CC   to the surface of the display system; and (b) identifying a BSD that
CC   binds to the predetermined epitope. The method is useful to identify bi-
CC   or multivalent polypeptides that comprise antibody binding sites capable
CC   of efficiently binding to the corresponding antigen. The polypeptides or
CC   antibodies identified by the method are useful therapeutically and
CC   diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC   fragments that bind independently of their position within bifunctional
CC   single-chain fusion proteins can be isolated from combinatorial antibody
CC   libraries using the new in vitro method
XX
SQ   Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;

  Query Match             98.5%;  Score 316.2;  DB 2;  Length 321;
  Best Local Similarity   99.1%;  Pred. No. 2.9e-93;
  Matches  318;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 3
AAV68539
ID   AAV68539 standard; DNA; 321 BP.
XX
AC   AAV68539;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Nucleotide sequence of human kappa 5.1 light chain variable region.
XX
KW   Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;
KW   auto-immune disease; graft rejection; allergy; inflammatory disease;
KW   endocrine disease; degenerative disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag= a
FT                   /product= "human kappa 5.1 light chain variable region"
XX
PN   WO9846645-A2.
XX
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PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-EP002180.
XX
PR 14-APR-1997; 97EP-00106109.
XX
PA (KUFE/) KUFER P.
PA (RAUM/) RAUM T.
XX
PI Kufer P, Raum T;
XX
DR WPI; 1998-594564/50.
DR P-PSDB; AAW68539.
XX
PT Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.
XX
PS Claim 9; Fig 9; 84pp; English.
XX
CC This is the nucleotide sequence of the human kappa light chain variable
CC region, used in the method of the invention. for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process
XX
SQ Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 U; 0 Other;

Query Match 79.6%; Score 255.4; DB 2; Length 321;
Best Local Similarity 87.2%; Pred. No. 2.6e-73;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  |||||||||| ||| ||||||||||||||||| || || |||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| ||||||| ||||| ||| | ||    | |||  ||| || |||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        301 GGGACACGACTGGACATTCAA 321
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RESULT 4
AAZ50588
ID AAZ50588 standard; DNA; 1630 BP.
XX
AC AAZ50588;
XX
DT 23-MAY-2000 (first entry)
XX
DE HD70scFv-Ck-interleukin 2 encoding DNA.
XX
KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
KW interleukin-2; Ck-domain; kappa light chain constant domain;
KW heterominibody; multifunctional compound; immunoglobulin; cytostatic;
KW immunostimulatory; antileukaemia; diagnosis; prevention;
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
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PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP005416.
XX
PR 28-JUL-1998; 98EP-00114082.
XX
PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR P-PSDB; AAY44995.
XX
PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis.
XX
PS Claim 8; Fig 55B; 166pp; English.
XX
CC The patent discloses heterominibodies which are multifunctional compounds
CC produceable in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heterominibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a DNA encoding right
CC chain of a heterominibody comprising HD70 single-chain Fv (scFv) fragment
CC N-terminally linked to human Ck domain (constant domain of immunoglobulin
CC -kappa light chain) which bears at its C-terminus the human inflammatory
CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
CC human epithelial cell adhesion molecule (EpCAM) also called 17-1A antigen
XX
SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;

Query Match 79.6%; Score 255.4; DB 3; Length 1630;
Best Local Similarity 87.2%; Pred. No. 5e-73;
Matches 280; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275
```

```
Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||| ||||| |  ||||||||| ||| |||||||||||||||||| || || |||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| ||||||| ||||| ||| | ||    | |||  ||| || |||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        396 GGGACACGACTGGACATTCAA 416
```

RESULT 5
AAZ50587
ID AAZ50587 standard; DNA; 1630 BP.
XX
AC AAZ50587;
XX
DT 23-MAY-2000 (first entry)
XX
DE HD70scFv-CH1-GM-CSF chain encoding DNA.
XX
KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
KW granulocyte/macrophage colony stimulating factor; heterominibody;
KW CH1-domain; multifunctional compound; heavy chain constant domain;
KW immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 39. .1610
FT /*tag= a
FT /product= "HD70scFv-CH1-GM-CSF chain"
FT misc_feature 96. .842
FT /*tag= b
FT /label= HD70_scFv
XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP005416.
XX
PR 28-JUL-1998; 98EP-00114082.
XX
PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR P-PSDB; AAY44994.
XX
PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis.
XX
PS Claim 8; Fig 55A; 166pp; English.
XX
CC The patent discloses heterominibodies which are multifunctional compounds
CC produceable in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heterominibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a DNA encoding left chain
CC of a heterominibody comprising HD70 single-chain Fv (scFv) fragment N-
CC terminally linked to human CH1 domain which bears at its C-terminus the
CC human inflammatory cytokine granulocyte/macrophage colony stimulating
CC factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
CC HD70 scFv specifically recognises the human epithelial cell adhesion
CC molecule (EpCAM) also called 17-1A antigen
XX
SQ Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

```
  Query Match           79.6%;  Score 255.4;  DB 3;  Length 1630;
  Best Local Similarity 87.2%;  Pred. No. 5e-73;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              ||||||| ||||| |  ||||||||| ||| |||||||||||||||||| || || |||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| ||||||| ||||| ||| | ||    | |||  ||| || |||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        396 GGGACACGACTGGACATTCAA 416
```

RESULT 6
AAT66781
ID AAT66781 standard; cDNA; 321 BP.
XX
AC AAT66781;
XX
DT 29-JAN-1998 (first entry)
XX
DE Anti-cancer specific antigen MAb light chain variable region cDNA.
XX
KW Light chain; variable region; cancer specific antigen; human;
KW monoclonal antibody; hMAb; diagnosis; cancer; immunotherapy;
KW purification; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT mat_peptide 1. .321
FT /*tag= a
XX
PN JP09098786-A.
XX
PD 15-APR-1997.
XX
PF 06-OCT-1995; 95JP-00284400.
XX
PR 06-OCT-1995; 95JP-00284400.
XX
PA (MOMI) MORINAGA & CO LTD.
PA (SHKJ) SHINGIJUTSU JIGYODAN.
XX

DR WPI; 1997-275445/25.
DR P-PSDB; AAW16649.
XX
PT cDNA encoding human monoclonal antibody - useful in medicine, or to
PT purify cancer specific antigen.
XX
PS Claim 2; Fig 2; 7pp; Japanese.
XX
CC The present sequence encodes the light chain variable region of an anti-
CC cancer specific antigen human monoclonal antibody (hMAb). The hMAb can be
CC used in medicine, e.g. clinical diagnosis of cancer or immunotherapy, or
CC to purify cancer specific antigen. The industrial scale production of
CC large amounts of the hMAb is made feasible by genetic engineering using
CC the hMAb cDNA
XX
SQ Sequence 321 BP; 86 A; 89 C; 72 G; 74 T; 0 U; 0 Other;

Query Match 76.6%; Score 245.8; DB 2; Length 321;
Best Local Similarity 85.4%; Pred. No. 3.6e-70;
Matches 274; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||| |||||| ||||| ||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCCGTCTGCATCTGTCGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||| ||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCACCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||       ||| |     | || | ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAACTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| ||||||||   | ||||||| ||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACAGTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321
```

RESULT 7
AAH74685
ID AAH74685 standard; DNA; 333 BP.
XX
AC AAH74685;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of the L chain variable region of ScFv3-4.
XX
KW Complementarity determining region; CDR; single chain antibody; ScFv;
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW envelope glycoprotein; ss.
XX
OS Homo sapiens.
XX
PN WO200158459-A1.
XX
PD 16-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-JP000967.
XX
PR 14-FEB-2000; 2000JP-00034906.
XX
PA (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
DR WPI; 2001-496986/54.
DR P-PSDB; AAG63656.
XX
PT Remedies for hepatitis C containing substances with antiviral effects
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT compounds, by inhibiting binding of hepatitis C virus envelope
PT glycoprotein or CD81.
XX
PS Claim 40; Page 119-120; 138pp; Japanese.
XX
CC The present sequence encodes the L chain variable region of a single
CC chain antibody of the invention. The specification describes a substance
CC can inhibit the binding between hepatitis C virus (HCV) and cells with
CC potential HCV infection, cells with expression of CD81, or CD81. This
CC substance is especially an antibody with affinity towards HCV E2/NS1
CC protein, containing amino acid sequences based on the complementarity
CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable
CC regions. The antibody inhibits the viral envelope glycoprotein. It is
CC also a CD81 inhibitor. The antibodies and drugs are used for treatment
CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C
XX
SQ Sequence 333 BP; 87 A; 89 C; 77 G; 80 T; 0 U; 0 Other;

Query Match 75.6%; Score 242.6; DB 5; Length 333;
Best Local Similarity 84.7%; Pred. No. 4.1e-69;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| ||||||||| ||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||       |||||    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| ||||||||    || ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321
```

RESULT 8
ABT34321
ID ABT34321 standard; DNA; 333 BP.
XX
AC ABT34321;
XX
DT 12-JUN-2003 (first entry)
XX
DE Hepatitis C virus treatment related human DNA sequence SEQ ID No 33.
XX
KW Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
KW antibody; recombinant; antiviral; infection; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003014728-A1.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-JP008175.

XX
PR 10-AUG-2001; 2001JP-00243947.
XX
PA (MITS-) MITSUBISHI PHARMA CORP.
PA (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX
PI Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
XX
DR WPI; 2003-248334/24.
XX
PT Pharmaceutical compositions for hepatitis C containing screened
PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
PT antibody, useful in preventing or treating HCV infections.
XX
PS Example 4; Page 88; 136pp; Japanese.
XX
CC The invention relates to a novel method for screening substances
CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
CC antibody having an affinity for the protein. The novel method comprises:
CC contacting the protein with any of the antibodies selected, from those
CC described in the specification, in the presence or absence of a test
CC substance; and comparing the binding results. Compositions comprising the
CC (recombinant) antibodies are useful as antivirals and are especially
CC useful in preventing or treating HCV (hepatitis C) infections. This
CC polynucleotide sequence represents a human DNA sequence relating to the
CC novel HCV therapy method of the invention
XX
SQ Sequence 333 BP; 87 A; 89 C; 77 G; 80 T; 0 U; 0 Other;

Query Match 75.6%; Score 242.6; DB 10; Length 333;
Best Local Similarity 84.7%; Pred. No. 4.1e-69;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| ||||||||| ||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||      |||||    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||   || ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321
```

RESULT 9
ABT34316
ID ABT34316 standard; DNA; 720 BP.
XX
AC ABT34316;
XX
DT 12-JUN-2003 (first entry)
XX
DE Hepatitis C virus treatment related human DNA sequence SEQ ID No 8.
XX
KW Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
KW antibody; recombinant; antiviral; infection; human; gene; ds.
XX
OS Homo sapiens.
XX

PN WO2003014728-A1.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-JP008175.
XX
PR 10-AUG-2001; 2001JP-00243947.
XX
PA (MITS-) MITSUBISHI PHARMA CORP.
PA (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX
PI Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
XX
DR WPI; 2003-248334/24.
XX
PT Pharmaceutical compositions for hepatitis C containing screened
PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
PT antibody, useful in preventing or treating HCV infections.
XX
PS Claim 11; Page 71-73; 136pp; Japanese.
XX
CC The invention relates to a novel method for screening substances
CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
CC antibody having an affinity for the protein. The novel method comprises:
CC contacting the protein with any of the antibodies selected, from those
CC described in the specification, in the presence or absence of a test
CC substance; and comparing the binding results. Compositions comprising the
CC (recombinant) antibodies are useful as antivirals and are especially
CC useful in preventing or treating HCV (hepatitis C) infections. This
CC polynucleotide sequence represents a human DNA sequence relating to the
CC novel HCV therapy method of the invention
XX
SQ Sequence 720 BP; 188 A; 196 C; 175 G; 161 T; 0 U; 0 Other;

Query Match 75.6%; Score 242.6; DB 10; Length 720;
Best Local Similarity 84.7%; Pred. No. 5.7e-69;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db         61 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 120

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| ||||||||| ||||| ||||||||||||||||||||||
Db        121 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 180

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||      |||||    | ||   ||||||||
Db        181 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 240

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        241 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 300

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||   || ||||||||||||||||||
Db        301 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 360

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        361 GGGACCAAGCTGGAGATCAAA 381
```

RESULT 10
AAH74689
ID AAH74689 standard; DNA; 900 BP.
XX
AC AAH74689;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of single chain antibody ScFv3-4.
XX

```
KW   Complementarity determining region; CDR; single chain antibody; ScFv;
KW   hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW   envelope glycoprotein; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .900
FT                   /*tag=  a
FT                   /product= "ScFv 3-4"
XX
PN   WO200158459-A1.
XX
PD   16-AUG-2001.
XX
PF   13-FEB-2001; 2001WO-JP000967.
XX
PR   14-FEB-2000; 2000JP-00034906.
XX
PA   (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI   Itami S,  Shibui T,  Seki M,  Yotsumoto Y,  Matsuura Y,  Miyamura T;
XX
DR   WPI; 2001-496986/54.
DR   P-PSDB; AAG63660.
XX
PT   Remedies for hepatitis C containing substances with antiviral effects
PT   e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT   compounds, by inhibiting binding of hepatitis C virus envelope
PT   glycoprotein or CD81.
XX
PS   Claim 38; Page 127-129; 138pp; Japanese.
XX
CC   The present sequence encodes a single chain antibody of the invention.
CC   The specification describes a substance can inhibit the binding between
CC   hepatitis C virus (HCV) and cells with potential HCV infection, cells
CC   with expression of CD81, or CD81. This substance is especially an
CC   antibody with affinity towards HCV E2/NS1 protein, containing amino acid
CC   sequences based on the complementarity determining region (CDR) 1, CDR2
CC   and CDR3 of the H and L chain variable regions. The antibody inhibits the
CC   viral envelope glycoprotein. It is also a CD81 inhibitor. The antibodies
CC   and drugs are used for treatment and/or prevention of hepatitis C, or for
CC   diagnosis of hepatitis C
XX
SQ   Sequence 900 BP; 198 A; 244 C; 259 G; 199 T; 0 U; 0 Other;

  Query Match           75.6%;  Score 242.6;  DB 5;  Length 900;
  Best Local Similarity   84.7%;  Pred. No. 6.3e-69;
  Matches  272;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db        496 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 555

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| ||||||||| ||||| ||||||||||||||||||||||
Db        556 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 615

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||       |||||    | ||   ||||||||
Db        616 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 675

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        676 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 735

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| ||||||||    || ||||||||||||||||||
Db        736 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 795

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        796 GGGACCAAGCTGGAGATCAAA 816
```

```
RESULT 11
ABT34325
ID   ABT34325 standard; DNA; 900 BP.
XX
AC   ABT34325;
XX
DT   12-JUN-2003  (first entry)
XX
DE   Hepatitis C virus treatment related human DNA sequence SEQ ID No 37.
XX
KW   Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
KW   antibody; recombinant; antiviral; infection; human; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003014728-A1.
XX
PD   20-FEB-2003.
XX
PF   09-AUG-2002; 2002WO-JP008175.
XX
PR   10-AUG-2001; 2001JP-00243947.
XX
PA   (MITS-) MITSUBISHI PHARMA CORP.
PA   (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX
PI   Itami S,  Seki M,  Kito M,  Matsuura Y,  Miyamura T;
XX
DR   WPI; 2003-248334/24.
XX
PT   Pharmaceutical compositions for hepatitis C containing screened
PT   inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
PT   antibody, useful in preventing or treating HCV infections.
XX
PS   Claim 1; Page 96-98; 136pp; Japanese.
XX
CC   The invention relates to a novel method for screening substances
CC   inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
CC   antibody having an affinity for the protein. The novel method comprises:
CC   contacting the protein with any of the antibodies selected, from those
CC   described in the specification, in the presence or absence of a test
CC   substance; and comparing the binding results. Compositions comprising the
CC   (recombinant) antibodies are useful as antivirals and are especially
CC   useful in preventing or treating HCV (hepatitis C) infections. This
CC   polynucleotide sequence represents a human DNA sequence relating to the
CC   novel HCV therapy method of the invention
XX
SQ   Sequence 900 BP; 198 A; 244 C; 259 G; 199 T; 0 U; 0 Other;

  Query Match           75.6%;  Score 242.6;  DB 10;  Length 900;
  Best Local Similarity   84.7%;  Pred. No. 6.3e-69;
  Matches  272;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db        496 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 555

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| ||||||||| ||||| ||||||||||||||||||||||
Db        556 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 615

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||       |||||    | ||   ||||||||
Db        616 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 675

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        676 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 735

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| ||||||||    || ||||||||||||||||||
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Db        736 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 795

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        796 GGGACCAAGCTGGAGATCAAA 816


RESULT 12
AAH68701
ID   AAH68701 standard; DNA; 321 BP.
XX
AC   AAH68701;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) antibody clone SH13 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93644.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 3; Col 74; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

  Query Match             74.5%;  Score 239.2;  DB 5;  Length 321;
  Best Local Similarity   84.8%;  Pred. No. 5.3e-68;
  Matches  268;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| |||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||      ||| |    |  |   ||||||||     | ||

Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              |||||||| || |||||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||||| |||||||||   | ||| ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 13
ACD45365
ID   ACD45365 standard; DNA; 321 BP.
XX
AC   ACD45365;
XX
DT   12-SEP-2003  (first entry)
XX
DE   Anti-Rh(D) light chain SH13 DNA.
XX
KW   Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW   magnetically activated cell sorting.
XX
OS   Homo sapiens.
XX
PN   US2003040605-A1.
XX
PD   27-FEB-2003.
XX
PF   04-MAY-2001; 2001US-00848798.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
PR   29-JAN-1999;   99US-00240274.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2003-512273/48.
DR   P-PSDB; ABO27451.
XX
PT   New human Rh(D)-binding protein useful for various diagnostic and
PT   therapeutic applications, including typing of blood or blood products.
XX
PS   Claim 12; Page 57; 187pp; English.
XX
CC   The invention relates to an isolated Rh(D) binding protein. The protein
CC   can be used for magnetically activated cell sorting. The protein is
CC   useful in various diagnostic and therapeutic applications in humans,
CC   including typing of blood or blood products. The present sequence
CC   represents DNA encoding a human anti-Rh(D) chain
XX
SQ   Sequence 321 BP; 84 A; 89 C; 74 G; 74 T; 0 U; 0 Other;

  Query Match             74.5%;  Score 239.2;  DB 9;  Length 321;
  Best Local Similarity   84.8%;  Pred. No. 5.3e-68;
  Matches  268;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| |||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122
```

```
Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||       ||| |    |  |   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||||| |||||||||    | ||| ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318
```

RESULT 14
AAH74684
ID AAH74684 standard; DNA; 333 BP.
XX
AC AAH74684;
XX
DT 29-OCT-2001 (first entry)
XX
DE Nucleotide sequence of the L chain variable region of ScFv3-3.
XX
KW Complementarity determining region; CDR; single chain antibody; ScFv;
KW hepatitis C virus; HCV; HCV infection; CD81; E2 protein; NS1 protein;
KW envelope glycoprotein; ss.
XX
OS Homo sapiens.
XX
PN WO200158459-A1.
XX
PD 16-AUG-2001.
XX
PF 13-FEB-2001; 2001WO-JP000967.
XX
PR 14-FEB-2000; 2000JP-00034906.
XX
PA (MITS-) MITSUBISHI-TOKYO PHARM INC.
XX
PI Itami S, Shibui T, Seki M, Yotsumoto Y, Matsuura Y, Miyamura T;
XX
DR WPI; 2001-496986/54.
DR P-PSDB; AAG63655.
XX
PT Remedies for hepatitis C containing substances with antiviral effects
PT e.g. antibodies, proteins, sulfated polysaccharides and low-molecular
PT compounds, by inhibiting binding of hepatitis C virus envelope
PT glycoprotein or CD81.
XX
PS Claim 40; Page 118-119; 138pp; Japanese.
XX
CC The present sequence encodes the L chain variable region of a single
CC chain antibody of the invention. The specification describes a substance
CC can inhibit the binding between hepatitis C virus (HCV) and cells with
CC potential HCV infection, cells with expression of CD81, or CD81. This
CC substance is especially an antibody with affinity towards HCV E2/NS1
CC protein, containing amino acid sequences based on the complementarity
CC determining region (CDR) 1, CDR2 and CDR3 of the H and L chain variable
CC regions. The antibody inhibits the viral envelope glycoprotein. It is
CC also a CD81 inhibitor. The antibodies and drugs are used for treatment
CC and/or prevention of hepatitis C, or for diagnosis of hepatitis C
XX
SQ Sequence 333 BP; 87 A; 91 C; 80 G; 75 T; 0 U; 0 Other;

Query Match 74.1%; Score 237.8; DB 5; Length 333;
Best Local Similarity 83.8%; Pred. No. 1.6e-67;
Matches 269; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||||| ||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||       ||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||||| || ||||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||    | ||||  |||||| |||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||| ||||||||||
Db        301 GGGACCAAGGTGGAGATCAAA 321
```

RESULT 15
ABT34320
ID ABT34320 standard; DNA; 333 BP.
XX
AC ABT34320;
XX
DT 12-JUN-2003 (first entry)
XX
DE Hepatitis C virus treatment related human DNA sequence SEQ ID No 32.
XX
KW Virucide; inhibit; binding; hepatitis C virus; HCV; E2/NS1 protein;
KW antibody; recombinant; antiviral; infection; human; gene; ds.
XX
OS Homo sapiens.
XX
PN WO2003014728-A1.
XX
PD 20-FEB-2003.
XX
PF 09-AUG-2002; 2002WO-JP008175.
XX
PR 10-AUG-2001; 2001JP-00243947.
XX
PA (MITS-) MITSUBISHI PHARMA CORP.
PA (NINA-) JAPAN AGENCY NAT INST HEALTH.
XX
PI Itami S, Seki M, Kito M, Matsuura Y, Miyamura T;
XX
DR WPI; 2003-248334/24.
XX
PT Pharmaceutical compositions for hepatitis C containing screened
PT inhibitors of binding between hepatitis virus (HCV) E2/NS1 protein and
PT antibody, useful in preventing or treating HCV infections.
XX
PS Example 4; Page 87; 136pp; Japanese.
XX
CC The invention relates to a novel method for screening substances
CC inhibiting the binding of hepatitis C virus (HCV) E2/NS1 protein to an
CC antibody having an affinity for the protein. The novel method comprises:
CC contacting the protein with any of the antibodies selected, from those
CC described in the specification, in the presence or absence of a test
CC substance; and comparing the binding results. Compositions comprising the
CC (recombinant) antibodies are useful as antivirals and are especially
CC useful in preventing or treating HCV (hepatitis C) infections. This
CC polynucleotide sequence represents a human DNA sequence relating to the
CC novel HCV therapy method of the invention
XX
SQ Sequence 333 BP; 87 A; 91 C; 80 G; 75 T; 0 U; 0 Other;

```
  Query Match             74.1%;  Score 237.8;  DB 10;  Length 333;
  Best Local Similarity   83.8%;  Pred. No. 1.6e-67;
  Matches  269;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||  || ||  ||       ||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||  |||||||||||||||||  |||||||||   | ||||  |||||| |||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||  ||||||||||
Db        301 GGGACCAAGGTGGAGATCAAA 321


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Job time : 274.757 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	239.2	74.5	321	3	US-09-240-274-199	Sequence 199, App
2	236.2	73.6	720	4	US-09-192-854-1	Sequence 1, Appli
3	236	73.5	321	3	US-09-240-274-113	Sequence 113, App
4	231.2	72.0	321	3	US-09-240-274-109	Sequence 109, App
5	229.6	71.5	321	3	US-09-240-274-102	Sequence 102, App
6	229.6	71.5	321	3	US-09-240-274-218	Sequence 218, App
7	228	71.0	321	3	US-09-240-274-107	Sequence 107, App
8	227.8	71.0	324	3	US-09-240-274-101	Sequence 101, App
9	227.8	71.0	324	3	US-09-240-274-112	Sequence 112, App
10	227.8	71.0	324	3	US-09-240-274-210	Sequence 210, App
11	226.6	70.6	714	4	US-09-472-087-62	Sequence 62, Appl
12	226.4	70.5	321	3	US-09-240-274-106	Sequence 106, App
13	226.4	70.5	321	3	US-09-240-274-108	Sequence 108, App
14	226.4	70.5	321	3	US-09-240-274-201	Sequence 201, App
15	226.4	70.5	321	3	US-09-240-274-203	Sequence 203, App
16	226.2	70.5	324	3	US-09-240-274-206	Sequence 206, App
17	225	70.1	321	2	US-08-378-939-13	Sequence 13, Appl
18	224.8	70.0	321	3	US-09-240-274-216	Sequence 216, App
19	224.8	70.0	321	3	US-09-240-274-221	Sequence 221, App
20	224.8	70.0	321	3	US-09-240-274-222	Sequence 222, App
21	223.2	69.5	321	3	US-09-240-274-104	Sequence 104, App
22	223.2	69.5	321	3	US-09-240-274-205	Sequence 205, App
23	223.2	69.5	321	3	US-09-240-274-211	Sequence 211, App
24	223	69.5	324	3	US-09-240-274-110	Sequence 110, App
25	221.6	69.0	321	3	US-09-240-274-105	Sequence 105, App
26	221	68.8	672	4	US-09-456-090A-47	Sequence 47, Appl
27	221	68.8	672	4	US-09-453-234-47	Sequence 47, Appl
28	220.2	68.6	324	2	US-08-378-939-23	Sequence 23, Appl
29	220	68.5	321	3	US-09-240-274-215	Sequence 215, App
30	220	68.5	321	3	US-09-240-274-217	Sequence 217, App
31	219.8	68.5	324	3	US-09-240-274-224	Sequence 224, App
32	218.6	68.1	321	3	US-08-599-226-36	Sequence 36, Appl
33	218.6	68.1	321	3	US-09-125-098-36	Sequence 36, Appl
34	218.6	68.1	321	4	US-09-540-018-36	Sequence 36, Appl
35	218.6	68.1	388	3	US-09-042-353-358	Sequence 358, App
36	218.6	68.1	388	3	US-08-758-417A-206	Sequence 206, App
37	218.4	68.0	402	4	US-09-472-087-49	Sequence 49, Appl
38	217.8	67.9	451	4	US-09-472-087-50	Sequence 50, Appl
39	217	67.6	321	1	US-08-488-376-12	Sequence 12, Appl
40	217	67.6	321	2	US-08-634-223-12	Sequence 12, Appl
41	217	67.6	321	2	US-08-634-224-12	Sequence 12, Appl
42	217	67.6	321	2	US-08-634-400-12	Sequence 12, Appl
43	217	67.6	321	2	US-08-635-878-12	Sequence 12, Appl
44	217	67.6	321	2	US-08-770-057-12	Sequence 12, Appl
45	217	67.6	321	3	US-09-335-697B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

Query Match 74.5%; Score 239.2; DB 3; Length 321;
Best Local Similarity 84.8%; Pred. No. 6.7e-72;
Matches 268; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

```
Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| ||||||||||||||||||||||||| ||||||||||||||||||||||| |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||      ||| |    | |   ||||||||      | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || |||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||||| |||||||||    | ||| ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
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                ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 2
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
;  APPLICANT: Winter, Greg
;  APPLICANT: Tomlinson, Ian
;  TITLE OF INVENTION: Methods for Selecting Functional Peptides
;  FILE REFERENCE: 3789/72916
;  CURRENT APPLICATION NUMBER: US/09/192,854
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/066,729
;  EARLIER FILING DATE: 1997-11-21
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-192-854-1

  Query Match             73.6%;  Score 236.2;  DB 4;  Length 720;
  Best Local Similarity   83.5%;  Pred. No. 1e-70;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||| ||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||  || || ||       ||| |     | ||   ||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||   | |||  | || || |||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||  ||||  ||||||
Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 3
US-09-240-274-113
; Sequence 113, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I13
US-09-240-274-113

  Query Match             73.5%;  Score 236;  DB 3;  Length 321;
  Best Local Similarity   84.2%;  Pred. No. 8.3e-71;
  Matches  266;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||| |||| |||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                 | |||||||| || || ||       ||| |     | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||||| ||||||||||  | |||  ||| |||||||| ||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACGGTACCCCTCACAGTTTTGGCCGGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 4
US-09-240-274-109
; Sequence 109, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-109

  Query Match             72.0%;  Score 231.2;  DB 3;  Length 321;
  Best Local Similarity   83.2%;  Pred. No. 3.6e-69;
  Matches  263;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||| |||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
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Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || |||||||||||| |||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTCCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || ||||||||| ||||||| ||| | |      ||||||||||||||||||||||
Db        243 TTTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCCGTACACTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 5
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

  Query Match             71.5%;  Score 229.6;  DB 3;  Length 321;
  Best Local Similarity   82.9%;  Pred. No. 1.3e-68;
  Matches  262;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| ||||||||||||||||||||   |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||      ||| |    | ||   |||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||| |||||||||    | || ||  || || ||||| |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              |||| |||| ||||||
Db        303 CAAGGTGGAAATCAAA 318


RESULT 6
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

  Query Match             71.5%;  Score 229.6;  DB 3;  Length 321;
  Best Local Similarity   82.9%;  Pred. No. 1.3e-68;
  Matches  262;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| ||||||||||||||||||||   |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||      ||| |    | ||   |||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || |||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||| |||||||||    | ||||  || || ||||| |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              |||| |||| ||||||
Db        303 CAAGGTGGAAATCAAA 318


RESULT 7
US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
```

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;  OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

  Query Match             71.0%;  Score 228;  DB 3;  Length 321;
  Best Local Similarity   82.6%;  Pred. No. 4.5e-68;
  Matches  261;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||||| ||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||       ||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||| |||||||||   | |||    ||||| |||   |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAACTTTCGGCGGAGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              |||| ||||||||||
Db        303 CAAGGTGGAGATCAAA 318


RESULT 8
US-09-240-274-101
; Sequence 101, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 101
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I01
US-09-240-274-101

  Query Match             71.0%;  Score 227.8;  DB 3;  Length 324;
  Best Local Similarity   84.3%;  Pred. No. 5.3e-68;
  Matches  269;  Conservative    0;  Mismatches   47;  Indels    3;  Gaps    1;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||| ||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||       ||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATC---CCGTACACTTTTGGCCAGGG 302
              || |||||||||||||||| |||||||||   | |   ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy        303 GACCAAGCTGGAGATCAAA 321
              ||||||||||||||||||
Db        303 GACCAAGCTGGAGATCAAA 321


RESULT 9
US-09-240-274-112
; Sequence 112, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 112
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I12
US-09-240-274-112

  Query Match             71.0%;  Score 227.8;  DB 3;  Length 324;
  Best Local Similarity   84.3%;  Pred. No. 5.3e-68;
  Matches  269;  Conservative    0;  Mismatches   47;  Indels    3;  Gaps    1;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||| ||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTATCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||       ||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATC---CCGTACACTTTTGGCCAGGG 302
              || |||||||||||||||| |||||||||   | |   ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGTACACTTTTGGCCAGGG 302

Qy        303 GACCAAGCTGGAGATCAAA 321
              ||||||||||||||||||
Db        303 GACCAAGCTGGAGATCAAA 321


RESULT 10
US-09-240-274-210
; Sequence 210, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
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;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 210
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH34
US-09-240-274-210

  Query Match             71.0%;  Score 227.8;  DB 3;  Length 324;
  Best Local Similarity   84.3%;  Pred. No. 5.3e-68;
  Matches  269;  Conservative    0;  Mismatches   47;  Indels    3;  Gaps    1;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||      |||      | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCGGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTAC---GACATCCCGTACACTTTTGGCCAGGG 302
              || |||||||||||||||| |||||||||     |  ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCCCGTACACTTTTGGCCAGGG 302

Qy        303 GACCAAGCTGGAGATCAAA 321
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Db        303 GACCAAGCTGGAGATCAAA 321


RESULT 11
US-09-472-087-62
; Sequence 62, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
;   LENGTH: 714
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-62

  Query Match             70.6%;  Score 226.6;  DB 4;  Length 714;
  Best Local Similarity   81.6%;  Pred. No. 2e-67;
  Matches  262;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||| |||||||| | ||||||||||||||||||||
Db        127 ATCACTTGCCGGGCAAGTCAGAGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCA 186

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||| || || || ||      ||| |    | ||  ||||||||
Db        187 GGGAAAGCCCCTAAACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 306

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| |||  ||||    |  || | |||||| ||||
Db        307 GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTTCGGCCCT 366

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              ||||||||  |||| ||||||
Db        367 GGGACCAAAGTGGAAATCAAA 387


RESULT 12
US-09-240-274-106
; Sequence 106, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I06
US-09-240-274-106

  Query Match             70.5%;  Score 226.4;  DB 3;  Length 321;
  Best Local Similarity   82.3%;  Pred. No. 1.6e-67;
  Matches  260;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||| ||||| ||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||| |||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||      ||| |    | ||  ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              ||||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
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Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||||| |||||||||    | ||||  ||| || ||||| |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
                  |||||||| |||
Db        303 ACGACTGGAGATTAAA 318


RESULT 13
US-09-240-274-108
; Sequence 108, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 108
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I08
US-09-240-274-108

  Query Match             70.5%;  Score 226.4;  DB 3;  Length 321;
  Best Local Similarity   82.3%;  Pred. No. 1.6e-67;
  Matches  260;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||| |||||||||||| ||||| |||||||||||||||||| ||
Db          3 CGAGCTCACCCAGTCTCCATTCTCCCTGTCTGCATCTGTCGGAGACAGAGTCACCATAAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| ||||||||| ||||||||| | || ||||||||||||||| ||||||||  |
Db         63 TTGCCGGGCAAGTCAGACCATTAGCAGGTCTTTAAATTGGTATCAGCATAAACCAGGGGA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||       ||| |  | | |    ||||||||   | | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTCTGCAGCGTGGGGTCCCACCCAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
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Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              | ||| ||||||| |||||| ||||||  |   |||||||||| ||||||||||||||
Db        243 CTTTGCGACTTACTTCTGTCAACAGAGTGTCAGAATCCCGTACAGTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 14
US-09-240-274-201
; Sequence 201, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 201
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH16
US-09-240-274-201

  Query Match             70.5%;  Score 226.4;  DB 3;  Length 321;
  Best Local Similarity   82.3%;  Pred. No. 1.6e-67;
  Matches  260;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||| |||||||||||| ||||| |||||||||||||||||| ||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCCTCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
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Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAACAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
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Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
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Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||||| |||||||||    | |||    ||||| |||   |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCAACTTTCGGCGGAGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              |||| ||||||||||||
Db        303 CAAGGTGGAGATCAAA 318


RESULT 15
US-09-240-274-203
; Sequence 203, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 203
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH20
US-09-240-274-203

  Query Match             70.5%;  Score 226.4;  DB 3;  Length 321;
  Best Local Similarity   82.3%;  Pred. No. 1.6e-67;
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  Matches  260;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||| |||||||||||| ||||| |||||||||||||||||| ||
Db          3 CGAGCTCACCCAGTCTCCATTCTCCCTGTCTGCATCTGTCGGAGACAGAGTCACCATAAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||| | || |||||||||||| || ||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGGTCTTTAAATTGGTATCAACATAAACCAGGGGA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||       ||| |  | | |    ||||||||   | | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTCTGCAGCGTGGGGTCCCACCCAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
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Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              | ||| ||||||| |||||| ||||||   |    |||||||||| ||||||||||||||
Db        243 CTTTGCGACTTACTTCTGTCAACAGAGTGTCAGAATCCCGTACAGTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


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Perfect score: 321
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Gapop 10.0 , Gapext 1.0

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19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	15	US-10-325-694-141	Sequence 141, App
2	255.4	79.6	321	15	US-10-325-694-147	Sequence 147, App
3	242.6	75.6	333	15	US-10-203-754A-61	Sequence 61, Appl
4	242.6	75.6	900	15	US-10-203-754A-65	Sequence 65, Appl
5	239.2	74.5	321	10	US-09-848-798-199	Sequence 199, App
6	237.8	74.1	333	15	US-10-203-754A-60	Sequence 60, Appl
7	237.8	74.1	900	15	US-10-203-754A-64	Sequence 64, Appl
8	236.2	73.6	324	17	US-10-344-514-3	Sequence 3, Appli
9	236.2	73.6	324	17	US-10-344-514-4	Sequence 4, Appli
10	236.2	73.6	720	9	US-09-192-854-1	Sequence 1, Appli
11	236.2	73.6	720	9	US-09-968-561A-1	Sequence 1, Appli
12	236.2	73.6	720	10	US-09-968-744A-1	Sequence 1, Appli
13	236.2	73.6	720	11	US-09-968-561A-1	Sequence 1, Appli
14	236.2	73.6	720	18	US-10-744-774-2	Sequence 2, Appli
15	236	73.5	321	10	US-09-848-798-113	Sequence 113, App
16	234.6	73.1	322	16	US-10-309-762-226	Sequence 226, App
17	234.6	73.1	322	16	US-10-309-762-227	Sequence 227, App
18	234.6	73.1	322	16	US-10-038-591-54	Sequence 54, Appl
19	234.6	73.1	322	18	US-10-775-444A-54	Sequence 54, Appl
20	234.6	73.1	729	15	US-10-216-484-125	Sequence 125, App
21	234.6	73.1	729	15	US-10-384-933-125	Sequence 125, App
22	233	72.6	322	16	US-10-309-762-221	Sequence 221, App
23	233	72.6	322	16	US-10-309-762-233	Sequence 233, App
24	231.4	72.1	321	17	US-10-663-244-78	Sequence 78, Appl
25	231.4	72.1	324	17	US-10-344-514-7	Sequence 7, Appli
26	231.4	72.1	324	17	US-10-344-514-8	Sequence 8, Appli
27	231.4	72.1	1106	16	US-10-264-049-121	Sequence 121, App
28	231.2	72.0	321	10	US-09-848-798-109	Sequence 109, App
29	229.8	71.6	324	18	US-10-409-814A-3	Sequence 3, Appli
30	229.8	71.6	384	16	US-10-309-762-115	Sequence 115, App
31	229.6	71.5	321	10	US-09-848-798-102	Sequence 102, App
32	229.6	71.5	321	10	US-09-848-798-218	Sequence 218, App
33	228.8	71.3	324	15	US-10-371-942-7	Sequence 7, Appli
34	228.8	71.3	324	15	US-10-371-942-19	Sequence 19, Appl
35	228.2	71.1	328	15	US-10-330-613-12	Sequence 12, Appl
36	228.2	71.1	328	15	US-10-330-530-12	Sequence 12, Appl
37	228.2	71.1	328	17	US-10-660-357-12	Sequence 12, Appl
38	228.2	71.1	387	9	US-09-905-243-27	Sequence 27, Appl
39	228	71.0	321	10	US-09-848-798-107	Sequence 107, App
40	227.8	71.0	324	10	US-09-848-798-101	Sequence 101, App
41	227.8	71.0	324	10	US-09-848-798-112	Sequence 112, App
42	227.8	71.0	324	10	US-09-848-798-210	Sequence 210, App
43	226.6	70.6	321	17	US-10-663-244-82	Sequence 82, Appl
44	226.6	70.6	714	14	US-10-153-382-18	Sequence 18, Appl
45	226.6	70.6	714	18	US-10-612-497-62	Sequence 62, Appl

ALIGNMENTS

RESULT 1
US-10-325-694-141
; Sequence 141, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
; LENGTH: 321
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-141

Query Match 100.0%; Score 321; DB 15; Length 321;
Best Local Similarity 100.0%; Pred. No. 3.1e-100;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
```

```
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
                |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 2
US-10-325-694-147
; Sequence 147, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
;  APPLICANT: KUFER, PETER
;  APPLICANT:  RAUM, TOBIAS
;  TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
;  TITLE OF INVENTION:  RECEPTORS AND USES THEREOF
;  FILE REFERENCE: 38164000
;  CURRENT APPLICATION NUMBER: US/10/325,694
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/403,107
;  PRIOR FILING DATE: 1999-10-14
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-325-694-147

  Query Match             79.6%;  Score 255.4;  DB 15;  Length 321;
  Best Local Similarity   87.2%;  Pred. No. 1.4e-77;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              |||||||| ||||| |  |||||||||| ||| |||||||||||||||||| || ||| |||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||    ||||| ||  ||
Db        301 GGGACACGACTGGACATTCAA 321


RESULT 3
US-10-203-754A-61
; Sequence 61, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
;  APPLICANT: ITAMI, Seima
;  APPLICANT:  SEKI, Makoto
;  APPLICANT:  MATSUURA, Yoshiharu
;  APPLICANT:  SHIBUI, Tatsurou
;  APPLICANT:  YOTSUMOTO, Yoshihisa
;  APPLICANT:  MIYAMURA, Tatsuo
;  TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
;  FILE REFERENCE: P22257
;  CURRENT APPLICATION NUMBER: US/10/203,754A
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: PCT/JP01/00967
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
;   LENGTH: 333
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-203-754A-61

  Query Match             75.6%;  Score 242.6;  DB 15;  Length 333;
  Best Local Similarity   84.7%;  Pred. No. 3.7e-73;
  Matches  272;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| |||||||| ||||| ||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||      |||||    | ||   |||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||||| || ||||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||    || ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 4
US-10-203-754A-65
; Sequence 65, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
;  APPLICANT: ITAMI, Seima
;  APPLICANT:  SEKI, Makoto
;  APPLICANT:  MATSUURA, Yoshiharu
;  APPLICANT:  SHIBUI, Tatsurou
;  APPLICANT:  YOTSUMOTO, Yoshihisa
;  APPLICANT:  MIYAMURA, Tatsuo
;  TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
;  FILE REFERENCE: P22257
;  CURRENT APPLICATION NUMBER: US/10/203,754A
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: PCT/JP01/00967
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
;   LENGTH: 900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-203-754A-65
```

```
  Query Match             75.6%;  Score 242.6;  DB 15;  Length 900;
  Best Local Similarity   84.7%;  Pred. No. 5.3e-73;
  Matches  272;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||  |||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db        496 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 555

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||| ||||||||| ||||| ||||||||||||||||||||
Db        556 ATCACTTGCCGGGCAAGTCAGCGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 615

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| ||  | ||       |||||     | ||   ||||||||
Db        616 GGGAAAGCCCCTAAGCTCCTGGTCTATGCTGCATCTAATTTGCAAAGTGGGGTCCCATCA 675

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        676 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 735

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||  |||||||||||||||||||  |||||||||    || ||||||||||||||||||
Db        736 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACACTATTCCGTACACTTTTGGCCAG 795

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        796 GGGACCAAGCTGGAGATCAAA 816


RESULT 5
US-09-848-798-199
; Sequence 199, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-848-798-199

  Query Match             74.5%;  Score 239.2;  DB 10;  Length 321;
  Best Local Similarity   84.8%;  Pred. No. 5.5e-72;
  Matches  268;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
              ||| ||| |||||||||||||||||||||||||| ||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
               | ||||||| || || ||       ||| |     |  |   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
              |||||||| || ||||||||||||||||||||||||||||||||||| ||||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              ||  |||||||||||||||||| |||||||||   | ||| ||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
              ||||||||||||||||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 6
US-10-203-754A-60
; Sequence 60, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
;  APPLICANT: ITAMI, Seima
;  APPLICANT:  SEKI, Makoto
;  APPLICANT:  MATSUURA, Yoshiharu
;  APPLICANT:  SHIBUI, Tatsurou
;  APPLICANT:  YOTSUMOTO, Yoshihisa
;  APPLICANT:  MIYAMURA, Tatsuo
;  TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
;  FILE REFERENCE: P22257
;  CURRENT APPLICATION NUMBER: US/10/203,754A
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: PCT/JP01/00967
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 333
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-203-754A-60

  Query Match             74.1%;  Score 237.8;  DB 15;  Length 333;
  Best Local Similarity   83.8%;  Pred. No. 1.7e-71;
  Matches  269;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||       ||| |     | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||  |||||||||||||||||||  |||||||||    | ||||  ||||||  |||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||  ||||||||||
Db        301 GGGACCAAGGTGGAGATCAAA 321


RESULT 7
US-10-203-754A-64
; Sequence 64, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
;  APPLICANT: ITAMI, Seima
;  APPLICANT:  SEKI, Makoto
;  APPLICANT:  MATSUURA, Yoshiharu
;  APPLICANT:  SHIBUI, Tatsurou
```

```
;  APPLICANT:  YOTSUMOTO, Yoshihisa
;  APPLICANT:  MIYAMURA, Tatsuo
;  TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
;  FILE REFERENCE: P22257
;  CURRENT APPLICATION NUMBER: US/10/203,754A
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: PCT/JP01/00967
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
;   LENGTH: 900
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-203-754A-64

  Query Match             74.1%;  Score 237.8;  DB 15;  Length 900;
  Best Local Similarity   83.8%;  Pred. No. 2.4e-71;
  Matches  269;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db        496 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 555

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db        556 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 615

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||||||  || || ||       ||| |    | ||   ||||||||
Db        616 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 675

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||||| ||||||
Db        676 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 735

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||  |||||||||||||||||  |||||||||    | ||||  |||||| |||
Db        736 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 795

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||| ||||||||||
Db        796 GGGACCAAGGTGGAGATCAAA 816


RESULT 8
US-10-344-514-3
; Sequence 3, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
;  APPLICANT: NAKASHIMA, Toshihiro et al.
;  TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
;  FILE REFERENCE: 0020-5111P
;  CURRENT APPLICATION NUMBER: US/10/344,514
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: JP 2001-177640
;  PRIOR FILING DATE: 2001-06-12
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-344-514-3

  Query Match             73.6%;  Score 236.2;  DB 17;  Length 324;
  Best Local Similarity   83.5%;  Pred. No. 6e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||||| |||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||||||  || || ||       ||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||  |||||||||||||||||  |||||||||    | ||||  |||||| |||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||| ||||||||||
Db        301 GGGACCAAGGTGGAGATCAAA 321


RESULT 9
US-10-344-514-4
; Sequence 4, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
;  APPLICANT: NAKASHIMA, Toshihiro et al.
;  TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
;  FILE REFERENCE: 0020-5111P
;  CURRENT APPLICATION NUMBER: US/10/344,514
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: JP 2001-177640
;  PRIOR FILING DATE: 2001-06-12
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 4
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(324)
US-10-344-514-4

  Query Match             73.6%;  Score 236.2;  DB 17;  Length 324;
  Best Local Similarity   83.5%;  Pred. No. 6e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  ||||| |||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||||||  || || ||       ||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||||| ||||||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||  |||||||||||||||||  |||||||||    | ||||  |||||| |||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 300

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||| ||||||||||
Db        301 GGGACCAAGGTGGAGATCAAA 321


RESULT 10
US-09-192-854-1
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```
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
;  APPLICANT: Winter, Greg
;  APPLICANT: Tomlinson, Ian
;  TITLE OF INVENTION: Methods for Selecting Functional Peptides
;  FILE REFERENCE: 3789/72916
;  CURRENT APPLICATION NUMBER: US/09/192,854
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/066,729
;  EARLIER FILING DATE: 1997-11-21
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-192-854-1

  Query Match             73.6%;  Score 236.2;  DB 9;  Length 720;
  Best Local Similarity   83.5%;  Pred. No. 8e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||||||||||||||| |||||||||    | |||  | || || |||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              ||||||||| |||| ||||||
Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 11
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
;  FILE REFERENCE: 8039/1073B
;  CURRENT APPLICATION NUMBER: US/09/968,561A
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: US 60/066,729
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/03135
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: US 09/511,939
;  PRIOR FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-561A-1

  Query Match             73.6%;  Score 236.2;  DB 9;  Length 720;
  Best Local Similarity   83.5%;  Pred. No. 8e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              |||||||||||||||||||| |||||||||    | |||  | || || |||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 12
US-09-968-744A-1
; Sequence 1, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
;  FILE REFERENCE: 8039/1073
;  CURRENT APPLICATION NUMBER: US/09/968,744A
;  CURRENT FILING DATE:  2003-01-13
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: US 60/066,729
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/03135
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: US 09/511,939
;  PRIOR FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-744A-1

  Query Match             73.6%;  Score 236.2;  DB 10;  Length 720;
  Best Local Similarity   83.5%;  Pred. No. 8e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516
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Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | ||||||||||| || ||||||||||||||||||||||||||||||||||||||| ||||||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||    | |||  | || || |||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 13
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Publication No. US20040038291A2
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
;  FILE REFERENCE: 8039/1073B
;  CURRENT APPLICATION NUMBER: US/09/968,561A
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
;  PRIOR APPLICATION NUMBER: US 60/066,729
;  PRIOR FILING DATE: 1997-11-21
;  PRIOR APPLICATION NUMBER: PCT/GB98/03135
;  PRIOR FILING DATE: 1998-10-20
;  PRIOR APPLICATION NUMBER: US 09/511,939
;  PRIOR FILING DATE: 2000-02-24
;  NUMBER OF SEQ ID NOS: 350
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-968-561A-1

  Query Match             73.6%;  Score 236.2;  DB 11;  Length 720;
  Best Local Similarity   83.5%;  Pred. No. 8e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
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Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 14
US-10-744-774-2
; Sequence 2, Application US/10744774
; Publication No. US20040219643A1
; GENERAL INFORMATION:
;  APPLICANT: Domantis Limited
;  APPLICANT:  Medical Research Council
;  APPLICANT:  Ignatovich, Olga
;  APPLICANT:  Jones, Philip C.
;  APPLICANT:  Tomlinson, Ian
;  APPLICANT:  Winter, Greg
;  TITLE OF INVENTION: Dual Specific Ligand
;  FILE REFERENCE: 8039/2102
;  CURRENT APPLICATION NUMBER: US/10/744,774
;  CURRENT FILING DATE:  2003-12-23
;  PRIOR APPLICATION NUMBER: PCT/GB02/03014
;  PRIOR FILING DATE: 2002-06-28
;  PRIOR APPLICATION NUMBER: GB 0115841.9
;  PRIOR FILING DATE: 2001-06-28
;  NUMBER OF SEQ ID NOS: 22
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: VH/HSA
US-10-744-774-2

  Query Match             73.6%;  Score 236.2;  DB 18;  Length 720;
  Best Local Similarity   83.5%;  Pred. No. 8e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||       ||| |    | ||   ||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||    | |||  | || || |||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 15
US-09-848-798-113
; Sequence 113, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
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;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 113
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I13
US-09-848-798-113

  Query Match             73.5%;  Score 236;  DB 10;  Length 321;
  Best Local Similarity   84.2%;  Pred. No. 7e-71;
  Matches  266;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCAC 65
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Qy         66 TTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGACA 125
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Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGGTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

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Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAGA 245
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Qy        246 TTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGAC 305
              || |||||||||||||||| ||||||||||  | |||  ||| |||||||| ||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACGGTACCCCTCACAGTTTTGGCCGGGGGAC 302

Qy        306 CAAGCTGGAGATCAAA 321
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GenCore version 5.1.6

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Title: US-09-403-107-141
Perfect score: 321
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
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6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	241	75.1	525	6	CD705928	CD705928 EST22455
5	239.4	74.6	447	2	AW405752	AW405752 UI-HF-BL0
6	238.6	74.3	608	2	AW404714	AW404714 UI-HF-BL0
7	238	74.1	854	5	BX397739	BX397739 BX397739
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25	233	72.6	750	6	CB985395	CB985395 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS CD690145 624 bp mRNA linear EST 25-JUN-2003
DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD690145
VERSION CD690145.1 GI:32210615
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"
ORIGIN

Query Match 76.1%; Score 244.2; DB 6; Length 624;
Best Local Similarity 85.0%; Pred. No. 8.1e-66;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db        114 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 173

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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Db        174 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 233

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        234 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 293

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Db        294 AGATTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 353

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Db        354 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAGAACTTTTGGCCAG 413

Qy        301 GGGACCAAGCTGGAGATCAAA 321

Db        414 GGGACCAAGCTGGAGATCAAA 434


RESULT 2
BG341239
LOCUS       BG341239                921 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602463904F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4576560 5',
            mRNA sequence.
ACCESSION   BG341239
VERSION     BG341239.1  GI:13147677
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 921)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1289  row: h  column: 01
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1. .921
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4576560"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             75.8%;  Score 243.4;  DB 4;  Length 921;
  Best Local Similarity   86.9%;  Pred. No. 1.6e-65;
  Matches  279;  Conservative    0;  Mismatches   41;  Indels    1;  Gaps    1;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Db         81 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 140

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120

Db        141 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 200

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180

Db        201 GGAAAGCC-CCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 259

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Db        260 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 319

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Db        320 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAG 379

Qy        301 GGGACCAAGCTGGAGATCAAA 321

Db        380 GGGACCAAGCTGGAGATCAAA 400


RESULT 3
AW405301
LOCUS       AW405301                487 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-ack-b-02-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3059259 5', mRNA sequence.
ACCESSION   AW405301
VERSION     AW405301.1  GI:6924358
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 487)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3059259"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_37"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

  Query Match             75.6%;  Score 242.6;  DB 2;  Length 487;
  Best Local Similarity   84.7%;  Pred. No. 2.4e-65;
  Matches  272;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Db         42 GACATCCAGATGACCCAGTCGCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 101

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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              |||||||| ||| ||||||||||||||||||||||||| ||||||||||||||||||||||
Db        102 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 161

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |   | ||||| || || |||||       ||| |     | ||   ||||||||
Db        162 GGGAAAGCCCCTAATCTCCTGATTTATGTTGCATCCATTTGCAAAGTGGGGTCCCATCA 221

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        222 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 281

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||      |||||||| ||||||||||
Db        282 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTGCCCCGTACAGTTTTGGCCAG 341

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||| |||||||||
Db        342 GGGACCAAGCTAGAGATCAAA 362


RESULT 4
CD705928
LOCUS       CD705928                525 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST22455 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD705928
VERSION     CD705928.1  GI:32236558
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 525)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
     source          1. .525
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             75.1%;  Score 241;  DB 6;  Length 525;
  Best Local Similarity   84.4%;  Pred. No. 7.9e-65;
  Matches  271;  Conservative    0;  Mismatches   50;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db        117 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 176

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db        177 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 236

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||       ||| |     | ||   ||||||||
Db        237 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 296

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || |||||||||||||||||||| |||||||||||||| ||||||
Db        297 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCGCCATCAGCAGTCTGCAACCT 356

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||| ||||||| |||||||||      |   ||||||||||||||
Db        357 GAAGATTTTGCAACTTACCACTGTCAACAGAGTTACAGTACGCCGTACACTTTTGGCCAG 416

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||| ||||||||||||
Db        417 CGGACCAACCTGGAGATCAAA 437


RESULT 5
AW405752
LOCUS       AW405752                447 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-abp-a-01-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3057288 5', mRNA sequence.
ACCESSION   AW405752
VERSION     AW405752.1  GI:6924809
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 447)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .447
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3057288"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_37"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

  Query Match             74.6%;  Score 239.4;  DB 2;  Length 447;
  Best Local Similarity   84.1%;  Pred. No. 2.4e-64;
  Matches  270;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db         83 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 142

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| |||||||||||||||| ||||
Db        143 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAGACCA 202

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||       ||| |     | |    ||||||||
Db        203 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAGAGTGGGGTCCCATCA 262

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || |||||||||||||||||||| |||||||||||||| ||||||
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Db        263 ACGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 322

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| ||||| |||    | |||||||| ||||||||||
Db        323 GAAGATTTTGCAACTTACTACTGTCAACAGAGCTACAGTACCCCGTACAGTTTTGGCCAG 382

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              ||||||||| ||||||||||
Db        383 GGGACCAAGGTGGAGATCAAA 403


RESULT 6
AW404714
LOCUS       AW404714                608 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-acd-c-11-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3058580 5', mRNA sequence.
ACCESSION   AW404714
VERSION     AW404714.1  GI:6923771
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 608)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .608
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3058580"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_37"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

  Query Match             74.3%;  Score 238.6;  DB 2;  Length 608;
  Best Local Similarity   84.5%;  Pred. No. 4.7e-64;
  Matches  268;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

Qy          5 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACCATCA 64
              ||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db         46 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 105

Qy         65 CTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCAGGAC 124
              |||| ||| |||||||||||||||||||||||| |||||||||||||||||| ||||
Db        106 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAATCAGGGA 165

Qy        125 AGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGACCGAT 184
              |  | ||||| || || || ||       ||| |    | ||   ||||||||     | |
Db        166 AAGCCCCTAACCTCCTGATCTATGCTGCATCCAGTTTGCAAAATGGGGTCCCATCAAGGT 225

Qy        185 TCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCTGAAG 244
              |||||||||| || |||||||||||||||||||||||||||||||||||| ||||||||||
Db        226 TCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAG 285

Qy        245 ATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAGGGGA 304
              ||| |||||||||| |||||||||||||| |   | |||||||| ||||||||||||||
Db        286 ATTTTGCAACTTACTTCTGTCAGCAGAGTTTCACTACCCCGTACAGTTTTGGCCAGGGGA 345

Qy        305 CCAAGCTGGAGATCAAA 321
              |||  ||||||||||||
Db        346 CCAGACTGGAGATCAAA 362


RESULT 7
BX397739
LOCUS       BX397739                854 bp    mRNA    linear   EST 28-APR-2004
DEFINITION  BX397739 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
            clone CS0DI041YP06 5-PRIME, mRNA sequence.
ACCESSION   BX397739
VERSION     BX397739.2  GI:46847409
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 854)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On May 13, 2003 this sequence version replaced gi:30617375.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
            end enriched, double-strand cDNA was digested with Not I and cloned
            into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
            was normalized. Library was constructed by Life Technologies, a
            division of Invitrogen. This sequence belongs to sequence cluster
            1696.r
            For more information about this cluster, see
            http://www.genoscope.cns.fr/cdna?s=CS0DI041DH03QP1&c=1696.r.
FEATURES             Location/Qualifiers
     source          1. .854
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DI041YP06"
                     /tissue_type="PLACENTA COT 25-NORMALIZED"
                     /clone_lib="Homo sapiens PLACENTA COT 25-NORMALIZED"
                     /note="1st strand cDNA was primed with a NotI-oligo(dT)
                     primer. Five prime end enriched, double-strand cDNA was
                     digested with Not I and cloned into the Not I and EcoR V
                     sites of the pCMVSPORT 6 vector. Library was normalized."
ORIGIN

  Query Match             74.1%;  Score 238;  DB 5;  Length 854;
  Best Local Similarity   85.7%;  Pred. No. 8.1e-64;
  Matches  276;  Conservative    0;  Mismatches   45;  Indels    1;  Gaps    1;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db         14 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 73

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||
Db         74 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 133

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||       ||| |    | ||   ||||||||
Db        134 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 193

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Db        194 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTCCAACCT 253

Qy        241 GAAGATT-CTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCA 299
              ||||||| |||||||||||||||||| |||||||||   | ||||||||||||||||||
Db        254 GAAGATTATTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCA 313

Qy        300 GGGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        314 GGGGACCAAGCTGGAGATCAAA 335


RESULT 8
AW407904
LOCUS       AW407904                422 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3061128 5', mRNA sequence.
ACCESSION   AW407904
VERSION     AW407904.1  GI:6926961
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 422)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .422
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3061128"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_37"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

  Query Match           74.1%;  Score 237.8;  DB 2;  Length 422;
  Best Local Similarity  83.8%;  Pred. No. 7.6e-64;
  Matches  269;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         23 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 82

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| ||||||||||||||||||||||
Db         83 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 142

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||      ||| |    | ||   ||||||||
Db        143 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 202

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||| || |||||||||||||||||||||||||||||||||| ||||||
Db        203 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 262

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||   | |||||  || || |||||
Db        263 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAA 322

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              ||||||||| |||| ||||||
Db        323 GGGACCAAGGTGGAAATCAAA 343


RESULT 9
AW404992
LOCUS       AW404992                391 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BL0-abx-a-03-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone
            IMAGE:3058060 5', mRNA sequence.
ACCESSION   AW404992
VERSION     AW404992.1  GI:6924049
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 391)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .391
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                     /mol_type="mRNA"
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                     /clone="IMAGE:3058060"
                     /tissue_type="lymph"
                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_37"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (1.5-2.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

  Query Match           73.6%;  Score 236.2;  DB 2;  Length 391;
  Best Local Similarity  83.5%;  Pred. No. 2.4e-63;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         65 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 124

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| |||||||||||||||||||||||| |||||||||||||||||| ||
Db        125 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAATCA 184

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||      ||| |    | ||   ||||||||
Db        185 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 244
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Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        245 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 304

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| ||||| |||||||||||||||||||||||    |||||     || || |||||
Db        305 GAAGATTTTGCAATTTACTACTGTCAGCAGAGTTACAGTATCCCTCCTACGTTCGGCCAA 364

Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        365 GGGACCAAGGTGGAAATCAAA 385
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RESULT 10
BM830977
LOCUS BM830977 671 bp mRNA linear EST 06-MAR-2002
DEFINITION K-EST0104754 S14K402s1 Homo sapiens cDNA clone S14K402s1-20-E05 5', mRNA sequence.
ACCESSION BM830977
VERSION BM830977.1 GI:19187386
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 671)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 20 row: E column: 05
High quality sequence stop: 671.
FEATURES Location/Qualifiers
source 1. .671
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402s1-20-E05"
/cell_line="K402"
/lab_host="Top10F'"
/clone_lib="S14K402s1"
/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI; Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library. After analyzing and sequencing about 2,000 ~ 3,000 colonies in original cDNA library, the abundant cDNAs were selected and amplified by PCR reaction using vector region primer including T7 promotor as 5' primer and N(dT)14 as 3' primer. The PCR products were used as template for synthesis of biotinylated single stranded RNA by in vitro transcription reaction. The synthesized RNA probes were hybridized with antisense single stranded cDNAs prepared from original liberary and incubated with avidin-gel. After removing DNA-RNA hybrids by centrifuge, the subtracted cDNA libraries were constructed by transformaion of the remaining DNA into competent cells E. coli Top10F' with electroporation method."

ORIGIN

Query Match 73.6%; Score 236.2; DB 4; Length 671;
Best Local Similarity 83.5%; Pred. No. 2.8e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
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Db         90 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAACTGTAGGAGACAGAGTCACC 149

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||| |||| ||| |||||||||| | |||| ||||| |||||||||||||||| ||||||
Db        150 ATCGCTTGCCGGGCAAGTCAGAGCGTCAGCAACTATTTAAATTGGTATCAGCAAAAACCA 209

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||      | |||||||| || || ||      ||| |     ||   |||||||
Db        210 GGGAGAGCCCCTAAGCTCCTTATCTATACTGTATCCAGTTTACAAAGTGGGGTCCCATCA 269

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
              | |||||||||||| || ||||||||||||||||||||||||||||||||||||||||||
Db        270 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 329

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||||| |||||||||    | ||||||||||||||||||
Db        330 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAG 389

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              ||||||||||||||||||||
Db        390 GGGACCAAGCTGGAGATCAAA 410
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RESULT 11
BM769909
LOCUS BM769909 684 bp mRNA linear EST 04-MAR-2002
DEFINITION K-EST0053259 S14K402 Homo sapiens cDNA clone S14K402-24-C07 5', mRNA sequence.
ACCESSION BM769909
VERSION BM769909.1 GI:19099524
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 684)
AUTHORS Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R., Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Kim,Y.S.
TITLE 21C Frontier Korean EST Project 2001
JOURNAL Unpublished (2002)
COMMENT Contact: Kim YS
Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
Email: yongsung@mail.kribb.re.kr
Plate: 24 row: C column: 07
High quality sequence stop: 684.
FEATURES Location/Qualifiers
source 1. .684
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="S14K402-24-C07"
/cell_line="K402"
/lab_host="Top10F'"
/clone_lib="S14K402"
/note="Organ: Stomach; Vector: pTZ18RP1; Site_1: EcoRI;

Site_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including EcoR I site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Top10F' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 4; Length 684;
Best Local Similarity 83.5%; Pred. No. 2.8e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||  |||| ||||||||||||||||
Db         90 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCAACTGTAGGAGACAGAGTCACC 149

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||| |||| ||| |||||||||| | |||| |||| ||||||||||||||| ||||||
Db        150 ATCGCTTGCCGGGCAAGTCAGAGCGTCAGCAACTATTTAAATTGGTATCAGCAAAAACCA 209

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||      | |||||||| || || ||      ||| |       ||   ||||||||
Db        210 GGGAGAGCCCCTAAGCTCCTTATCTATACTGTATCCAGTTTACAAAGTGGGGTCCCATCA 269

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | |||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        270 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 329

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| ||||||||   | ||||||||||||||||||||
Db        330 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTACACTTTTGGCCAG 389

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||||||||||||||||
Db        390 GGGACCAAGCTGGAGATCAAA 410
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RESULT 12
CD684441
LOCUS CD684441 693 bp mRNA linear EST 25-JUN-2003
DEFINITION EST961 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD684441
VERSION CD684441.1 GI:32199435
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 693)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
source 1. .693
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 693;
Best Local Similarity 83.5%; Pred. No. 2.8e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||  |||| ||||||||||||||||
Db        120 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACC 179

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||||||| ||| |||| |||||||||||| |||||| ||||||||||||||||||||||
Db        180 ATCACTTGCCGGGCAAGCCAGAGCATTAGCCGCTATTTAAATTGGTATCAGCAGAAACCA 239

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||  |   ||| |    | ||   ||||||||
Db        240 GGGAAAGCCCCTAAGCTCCTGATCTATGGTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 299

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | |||||||||| || ||||||||||||||||||||||||||||||||||| ||||||
Db        300 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 359

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
              ||||||| |||||||||||||||| ||||||||||   | |||    ||| || |||
Db        360 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACGGTACCCCCCTCACCTTCGGCGGA 419

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              |||||||| ||||||||||
Db        420 GGGACCAAGGTGGAGATCAAA 440
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RESULT 13
CB984723
LOCUS CB984723 742 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT_13460684 NIH_MGC_184 Homo sapiens cDNA clone IMAGE:30325808 5', mRNA sequence.
ACCESSION CB984723
VERSION CB984723.1 GI:30279247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 742)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM132 row: d column: 09
High quality sequence stop: 453.
FEATURES Location/Qualifiers
source 1. .742
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:30325808"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc);

Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 742;
Best Local Similarity 83.5%; Pred. No. 2.9e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db         93 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 152

Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
              ||||||||| ||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        153 ATCACTTGCCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 212

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||| |  | ||||| || || |||||      ||| |    | ||   ||||||||
Db        213 GGAAAAGCCCCTAACCTCCTGATTTATGCTGCATCCAGTTTGCAAGGTGGGGTCCCATCA 272

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
               | ||||||||||| || ||||||||||||||||||||||||||||||| | ||||||
Db        273 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTTTGCAACCT 332

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
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Db        333 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTGCCCCTTACACTTTCGGCCCT 392

Qy        301 GGGACCAAGCTGGAGATCAAA 321
              || |||||  |||| ||||||
Db        393 GGAACCAATGTGGATATCAAA 413
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RESULT 14
CB956867
LOCUS CB956867 748 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT_13778741 NIH_MGC_184 Homo sapiens cDNA clone IMAGE:30351770 5', mRNA sequence.
ACCESSION CB956867
VERSION CB956867.1 GI:30212984
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 748)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM149 row: n column: 03
High quality sequence stop: 528.
FEATURES Location/Qualifiers
source 1. .748
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30351770"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 748;
Best Local Similarity 83.5%; Pred. No. 2.9e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        215 GGGAAAGCCCCTAACCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 274

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
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Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        395 GGGACCAAGCTGGAGATCAAA 415
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RESULT 15
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LOCUS CB986767 754 bp mRNA linear EST 01-MAY-2003
DEFINITION AGENCOURT_13647493 NIH_MGC_184 Homo sapiens cDNA clone IMAGE:30329383 5', mRNA sequence.
ACCESSION CB986767
VERSION CB986767.1 GI:30281287
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 754)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

Plate: NDCM141 row: i column: 08
High quality sequence stop: 557.

FEATURES Location/Qualifiers
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ORIGIN

Query Match 73.6%; Score 236.2; DB 6; Length 754;
Best Local Similarity 83.5%; Pred. No. 2.9e-63;
Matches 268; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

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Qy         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120
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Db        154 ATTACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 213

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||      ||| |    | ||   |||||||| |
Db        214 GGGAATGCCCCTAAGCTCCTGATCTATGTTGCATCCAGTTTGCAAAGTGGGGTCCCAGCA 273

Qy        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240
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Db        274 AGGTTCAGCGGCAGTGGATCTGGGACAGCTTTCACTCTCACCATCAGCAGTCTGCAACCT 333

Qy        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300
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Qy        301 GGGACCAAGCTGGAGATCAAA 321
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Db        394 GGGACCAAGGTGGAGATCAAA 414
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Search completed: December 7, 2004, 11:13:45
Job time : 1876.31 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 02:37:53 ; Search time 2155.18 Seconds
(without alignments)
8360.047 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
Perfect score: 381
Sequence: 1 gaggtgcagctgctcgagtc.....ccacggtcaccgtctcctca 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379.4	99.6	381	6	AX003759	AX003759 Sequence
2	379.4	99.6	381	6	BD139667	BD139667 A novel m
3	379.4	99.6	414	6	A84376	A84376 Sequence 14
4	379.4	99.6	414	6	BD075294	BD075294 Novel met
5	378.4	99.3	1630	6	BD222938	BD222938 Heteromin
6	378.4	99.3	1630	6	BD222939	BD222939 Heteromin
7	378.4	99.3	1630	6	AX023365	AX023365 Sequence
8	378.4	99.3	1630	6	AX023367	AX023367 Sequence
9	351.2	92.2	438	9	HSROU127	X81745 H.sapiens r
10	336.8	88.4	378	9	HSA579147	AJ579147 Homo sapi
11	336.8	88.4	378	9	HSA579148	AJ579148 Homo sapi
12	330.8	86.8	376	9	AB021535	AB021535 Homo sapi
13	330.4	86.7	381	9	AJ627232	AJ627232 Homo sapi
14	325.4	85.4	384	9	HSBUD94H	Z46379 Homo sapien
15	324.8	85.2	360	9	AY607468	AY607468 Homo sapi
16	324.4	85.1	1413	6	BD185289	BD185289 Uses of a
17	324.4	85.1	1413	6	BD273725	BD273725 Human mon
18	324.4	85.1	1413	6	AR454402	AR454402 Sequence
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20	324.2	85.1	391	9	AB021524	AB021524 Homo sapi
21	324	85.0	379	9	HSA239331	AJ239331 Homo sapi
22	323.8	85.0	384	9	HSA239336	AJ239336 Homo sapi
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24	323.2	84.8	429	6	E35220	E35220 Human monoc
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27	321.6	84.4	369	9	AF062302	AF062302 Homo sapi
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34	320.8	84.2	379	9	AB021507	AB021507 Homo sapi
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36	320.4	84.1	435	9	AF431051	AF431051 Homo sapi
37	320.2	84.0	390	9	AB063901	AB063901 Homo sapi
38	320.2	84.0	424	12	AF453033	AF453033 Synthetic
39	319.6	83.9	368	9	HSVH3182	X62970 H.sapiens r
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44	318.4	83.6	429	6	E35212	E35212 Human monoc
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ALIGNMENTS

RESULT 1
AX003759
LOCUS AX003759 381 bp DNA linear PAT 24-AUG-2000
DEFINITION Sequence 53 from Patent WO9925818.
ACCESSION AX003759
VERSION AX003759.1 GI:9927566
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Kufer,P. and Raum,T.
TITLE Method of identifying binding site domains that retain the capacity of binding to an epitope
JOURNAL Patent: WO 9925818-A 53 27-MAY-1999;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES Location/Qualifiers
source 1. .381
/organism="Homo sapiens"
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ORIGIN

Query Match 99.6%; Score 379.4; DB 6; Length 381;
Best Local Similarity 99.7%; Pred. No. 1.3e-108;
Matches 380; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Qy        361 ACCACGGTCACCGTCTCCTCA 381
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Db        361 ACCACGGTCACCGTCTCCTCA 381


RESULT 2
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LOCUS       BD139667                381 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  A novel method of identifying binding site domains that retain the
            capacity of binding to an epitope.
ACCESSION   BD139667
VERSION     BD139667.1  GI:23234612
KEYWORDS    JP 2002508924-A/52.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 381)
  AUTHORS   Kufer,P., Raum,T., Borschert,K., Zettl,F. and Lutterbuese,R.
  TITLE     A novel method of identifying binding site domains that retain the
            capacity of binding to an epitope
  JOURNAL   Patent: JP 2002508924-A 52 26-MAR-2002;
            PETER KUFER
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508924-A/52
            PD   26-MAR-2002
            PF   16-NOV-1998 JP 2000521184
            PR   17-NOV-1997 EP   97120096.9
            PI   PETER KUFER,TOBIAS RAUM,KATRIN BORSCHERT,FLORIAN ZETTL,RALF
            PI   LUTTERBUESE
            PC   C12N15/09,A61K38/00,A61K38/22,A61K38/43,A61K39/395,C07K14/705,
            PC   C07K16/30,
            PC   C12N1/21,C12N5/10,C12P21/02,C12P21/08,G01N33/566,C12N15/00, PC
              A61K37/02,
            PC   A61K37/24,A61K37/48,C12N5/00
            CC   A novel method of identifying binding site
            domains that retain
            CC          the
            CC   capacity of binding to an epitope
            FH   Key             Location/Qualifiers
            FT   source          1. .381
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
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ORIGIN

  Query Match             99.6%;  Score 379.4;  DB 6;  Length 381;
  Best Local Similarity   99.7%;  Pred. No. 1.3e-108;
  Matches  380;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        361 ACCACGGTCACCGTCTCCTCA 381


RESULT 3
A84376
LOCUS       A84376                  414 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 143 from Patent WO9846645.
ACCESSION   A84376
VERSION     A84376.1  GI:6733299
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
            USES THEREOF
  JOURNAL   Patent: WO 9846645-A 143 22-OCT-1998;
            KUFER PETER (DE); RAUM TOBIAS (DE)
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                      GSGWRPYYYYGMDVWGQGTTVTVSSAPTKAPDVFPL"
ORIGIN

  Query Match             99.6%;  Score 379.4;  DB 6;  Length 414;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-108;
  Matches  380;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
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Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
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Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        361 ACCACGGTCACCGTCTCCTCA 381


RESULT 4
BD075294
LOCUS       BD075294                 414 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel method for the production of anti-human antigen receptors and
            uses thereof.
ACCESSION   BD075294
VERSION     BD075294.1  GI:22620897
KEYWORDS    JP 2001519824-A/23.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 414)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Novel method for the production of anti-human antigen receptors and
            uses thereof
  JOURNAL   Patent: JP 2001519824-A 23 23-OCT-2001;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001519824-A/23
            PD   23-OCT-2001
            PF   14-APR-1998 JP 1998543494
            PR   14-APR-1997 EP   97106109.8
            PI   PETER KUFER,TOBIAS RAUM
            PC   C07K16/00,C07K16/30,A61K39/395
            CC   Novel method for the production of anti-human antigen  CC
                  receptors and uses
            CC   thereof
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ORIGIN

  Query Match           99.6%;  Score 379.4;  DB 6;  Length 414;
  Best Local Similarity   99.7%;  Pred. No. 1.4e-108;
  Matches  380;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Db        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        361 ACCACGGTCACCGTCTCCTCA 381


RESULT 5
BD222938
LOCUS       BD222938                 1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222938
VERSION     BD222938.1  GI:33032708
KEYWORDS    JP 2002521053-A/32.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 32 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/32
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC   (C12N5/00,C12R1:91)
            CC   Heterominibodies
            FH   Key             Location/Qualifiers
            FT   CDS             (39). .(1607).
FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           99.3%;  Score 378.4;  DB 6;  Length 1630;
  Best Local Similarity   99.7%;  Pred. No. 3.3e-108;
  Matches  379;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        462 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 521

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 581

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 641

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 701

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 761

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        762 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 821

Qy        361 ACCACGGTCACCGTCTCCTC 380
              ||||||||||||||||||||
Db        822 ACCACGGTCACCGTCTCCTC 841


RESULT 6
BD222939
LOCUS       BD222939               1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222939
VERSION     BD222939.1  GI:33032709
KEYWORDS    JP 2002521053-A/33.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 33 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/33
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC   (C12N5/00,C12R1:91)
            CC   Heterominibodies
            FH   Key             Location/Qualifiers
            FT   CDS             (39). .(1610).
FEATURES              Location/Qualifiers
     source           1. .1630
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             99.3%;  Score 378.4;  DB 6;  Length 1630;
  Best Local Similarity   99.7%;  Pred. No. 3.3e-108;
  Matches  379;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        462 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 521

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 581

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 641

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 701

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 761

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        762 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 821

Qy        361 ACCACGGTCACCGTCTCCTC 380
              ||||||||||||||||||||
Db        822 ACCACGGTCACCGTCTCCTC 841


RESULT 7
AX023365
LOCUS       AX023365               1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 36 from Patent WO0006605.
ACCESSION   AX023365
VERSION     AX023365.1  GI:10183777
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 36 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
FEATURES              Location/Qualifiers
     source           1. .1630
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     CDS              39. .1610
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAC08835.1"
                      /db_xref="GI:10183778"
                      /translation="MGWSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
                      SQSISSYLNWYQQKPGQPPKLLIYWASTRESGVPDRFSGSESGTNYTLTISSLQPEDF
                      ATYFCQQSDSLPITFGQGTRLDIQGGGGSGGGGSGGGGSEVQLLESGGGVVQPGRSLR
                      LSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN
                      TLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTTVTVSSGTPLGDTT
                      HTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                      LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTSGGGGSAP
                      ARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                      LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIP
                      FDCWEPVQEHHHHHH"
ORIGIN

  Query Match             99.3%;  Score 378.4;  DB 6;  Length 1630;
  Best Local Similarity   99.7%;  Pred. No. 3.3e-108;
  Matches  379;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        462 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 521

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 581

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 641

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 701

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 761

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        762 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 821

Qy        361 ACCACGGTCACCGTCTCCTC 380
              ||||||||||||||||||||
Db        822 ACCACGGTCACCGTCTCCTC 841


RESULT 8
AX023367
LOCUS       AX023367               1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 38 from Patent WO0006605.
ACCESSION   AX023367
VERSION     AX023367.1  GI:10183779
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 38 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             39. .1613
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC08836.1"
                     /db_xref="GI:10183780"
                     /translation="MGWSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
                     SQSISSYLNWYQQKPGQPPKLLIYWASTRESGVPDRFSGSESGTNYTLTISSLQPEDF
                     ATYFCQQSDSLPITFGQGTRLDIQGGGGSGGGGSGGGGSEVQLLESGGGVVQPGRSLR
                     LSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN
                     TLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTTVTVSSGTPLGDTT
                     HTRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
                     TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGSA
                     PTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL
                     EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF
                     LNRWITFCQSIISTLT"
ORIGIN

  Query Match           99.3%;  Score 378.4;  DB 6;  Length 1630;
  Best Local Similarity 99.7%;  Pred. No. 3.3e-108;
  Matches  379;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        462 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 521

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        522 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 581

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        582 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 641

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        642 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 701

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        702 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 761

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        762 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 821

Qy        361 ACCACGGTCACCGTCTCCTC 380
              ||||||||||||||||||||
Db        822 ACCACGGTCACCGTCTCCTC 841


RESULT 9
HSROU127
LOCUS       HSROU127               438 bp    mRNA    linear   PRI 29-FEB-1996
DEFINITION  H.sapiens rearranged VDJ region (ROU127).
ACCESSION   X81745
VERSION     X81745.1  GI:1212972
KEYWORDS    diversity region; immunoglobulin heavy chain; joining region;
            variable region; VH-3 family.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Milili,M., Schiff,C., Fougereau,M. and Tonnelle,C.
  TITLE     The VDJ repertoire expressed in human preB cells reflects the
            selection of bona fide heavy chains
  JOURNAL   Eur. J. Immunol. 26 (1), 63-69 (1996)
  MEDLINE   96152725
   PUBMED   8566085
REFERENCE   2  (bases 1 to 438)
  AUTHORS   Tonnelle,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (15-SEP-1994) C. Tonnelle, Centre d'Immunologie
            Marseille-Luminy, Case 906, 13288 Marseille, Cedex 9, FRANCE
COMMENT     Related sequences: X65741, X65883 to X65920.
FEATURES             Location/Qualifiers
     source          1. .438
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="ROU 127"
                     /cell_type="pre B-lymphocytes"
                     /tissue_type="bone marrow"
                     /clone_lib="ROU"
                     /rearranged
     sig_peptide     1. .57
     V_region        58. .353
                     /product="immunoglobulin heavy chain V region"
     D_segment       354. .376
                     /product="immunoglobulin heavy chain D segment"
     J_segment       377. .438
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ORIGIN

  Query Match           92.2%;  Score 351.2;  DB 9;  Length 438;
  Best Local Similarity 95.3%;  Pred. No. 1.1e-99;
  Matches  362;  Conservative    0;  Mismatches   18;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Db        299 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAAAGGG 358

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || ||  |    || ||     ||||||||||||||||||||||||||||||||||||||
Db        359 GGCGGTTCCCCCGCCGGCATTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 418

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        419 CCACGGTCACCGTCTCCTCA 438


RESULT 10
HSA579147
LOCUS       HSA579147               378 bp    mRNA    linear   PRI 01-JUN-2004
DEFINITION  Homo sapiens partial mRNA for IgM immunoglobulin heavy chain
            variable region (IGHV3-30 gene), clone T2.3.9.
ACCESSION   AJ579147
VERSION     AJ579147.1  GI:47846472
KEYWORDS    IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dono,M.
  TITLE     Characterization of a novel CD5+ B cell population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 378)
  AUTHORS   Dono,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2003) Dono M., Oncologia Medica C., Istituto
            Nazionale Ricerca sul Cancro, L. go R. Benzi 10, Genova, 16132,
            ITALY
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="T2.3.9"
                     /tissue_type="tonsil"
                     /rearranged
                     /country="Italy:Genova"
     gene            1. .378
                     /gene="IGHV3-30"
     CDS             <1. .>378
                     /gene="IGHV3-30"
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="CAE45401.1"
                     /db_xref="GI:47846473"
                     /translation="QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKG
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                     /product="immunoglobulin heavy chain variable region"
ORIGIN

  Query Match             88.4%;  Score 336.8;  DB 9;  Length 378;
  Best Local Similarity   94.7%;  Pred. No. 4e-95;
  Matches  360;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---C 298

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
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Db        299 AGTATTACTATGATGGGAAATACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 11
HSA579148
LOCUS       HSA579148               378 bp    mRNA    linear   PRI 01-JUN-2004
DEFINITION  Homo sapiens partial mRNA for IgM immunoglobulin heavy chain
            variable region (IGHV3-30 gene), clone T2.3.10.
ACCESSION   AJ579148
VERSION     AJ579148.1  GI:47846474
KEYWORDS    IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dono,M.
  TITLE     Characterization of a novel CD5+ B cell population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 378)
  AUTHORS   Dono,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (07-MAY-2003) Dono M., Oncologia Medica C., Istituto
            Nazionale Ricerca sul Cancro, L. go R. Benzi 10, Genova, 16132,
            ITALY
FEATURES             Location/Qualifiers
     source          1. .378
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /chromosome="14"
                     /clone="T2.3.10"
                     /tissue_type="tonsil"
                     /rearranged
                     /country="Italy:Genova"
     gene            1. .378
                     /gene="IGHV3-30"
     CDS             <1. .>378
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                     /codon_start=1
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                     YDGKYYYYYGMDVWGQGTTVTVSS"
     V_region        <1. .>378
                     /gene="IGHV3-30"
                     /product="immunoglobulin heavy chain variable region"
ORIGIN

  Query Match             88.4%;  Score 336.8;  DB 9;  Length 378;
  Best Local Similarity   94.7%;  Pred. No. 4e-95;
  Matches  360;  Conservative    0;  Mismatches   17;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
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Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
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Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---C 298

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
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Db        299 AGTATTACTATGATGGGAAATACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
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Db        359 CCACGGTCACCGTCTCCTCA 378
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RESULT 12
AB021535
LOCUS       AB021535                376 bp    mRNA    linear   PRI 27-MAR-2002
DEFINITION  Homo sapiens mRNA for immunoglobulin heavy chain variable region
            (IgM), partial cds, clone krpbmc46.
ACCESSION   AB021535
VERSION     AB021535.1  GI:4107083
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Hakoda,M., Taniguchi,A., Kotake,S., Higami,K., Ichikawa,N.,
            Silverman,G.J. and Kamatani,N.
  TITLE     Pathogenic implication of a prototype B cell superantigen,
            staphylococcal protein A, in rheumatoid arthritis
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 376)
  AUTHORS   Hakoda,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (18-DEC-1998) Masayuki Hakoda, Tokyo Women's Medical
            University, Institute of Rheumatology; 10-22 Kawada-cho
            Shinjuku-ku, Tokyo 162-0054, Japan
            (E-mail:ratokyo@momo.so-net.or.jp, Tel:81-3-5269-1725,
            Fax:81-3-5269-1726)
FEATURES             Location/Qualifiers
     source          1. .376
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                     /clone="krpbmc46"
                     /cell_type="B cell"
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                     /product="immunoglobulin heavy chain variable region
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                     /db_xref="GI:4107084"
                     /db_xref="IMGT/LIGM:AB021535"
                     /translation="QVQLVESGGGVVQPGRSLKLSCAASGFTFSSYGMHWVRQAPGKG
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ORIGIN
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  Query Match           86.8%;  Score 330.8;  DB 9;  Length 376;
  Best Local Similarity   93.9%;  Pred. No. 3.2e-93;
  Matches  357;  Conservative    0;  Mismatches   17;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAAACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
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Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---- 297

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
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Db        298 --TGGCAAGTGGCTACGATGCGCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 355

Qy        362 CCACGGTCACCGTCTCCTCA 381
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Db        356 CCACGGTCACCGTCTCCTCA 375
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RESULT 13
AJ627232
LOCUS       AJ627232                381 bp    mRNA    linear   PRI 30-JUN-2004
DEFINITION  Homo sapiens partial mRNA for IgD immunoglobulin heavy chain
            variable region (IGHV3-30 gene), clone T3.3.5.
ACCESSION   AJ627232
VERSION     AJ627232.1  GI:49523837
KEYWORDS    IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Dono,M.
  TITLE     Characterization of a novel CD5+ B cell population
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 381)
  AUTHORS   Dono,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-FEB-2004) Dono M., Oncologia Medica C, Istituto
            Nazionale Ricerca sul Cancro, L.go R. Benzi 10, Italy, 16132, ITALY
FEATURES             Location/Qualifiers
     source          1. .381
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                     /chromosome="14"
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                     /tissue_type="tonsil"
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     gene            1. .381
                     /gene="IGHV3-30"
     CDS             <1. .>381
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     V_region        <1. .>381
                     /gene="IGHV3-30"
                     /product="immunoglobulin heavy chain variable region"
ORIGIN

  Query Match             86.7%;  Score 330.4;  DB 9;  Length 381;
  Best Local Similarity   91.8%;  Pred. No. 4.2e-93;
  Matches  349;  Conservative    0;  Mismatches   31;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
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Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGGGGCAA 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                  || |  |  |   || |||||    ||||||||||||||||||||||||||||
Db        302 TAGATTATTGTAGTGGTGGTAGCTGCTACTCTGGCGGTATGGACGTCTGGGGCCAAGGGA 361

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        362 CCACGGTCACCGTCTCCTCA 381


RESULT 14
HSBUD94H
LOCUS       HSBUD94H                384 bp    mRNA    linear   PRI 28-OCT-1994
DEFINITION  Homo sapiens mRNA for anti-Sm antibody VH chain (VH3/Dxp4/JH6).
ACCESSION   Z46379
VERSION     Z46379.1  GI:587147
KEYWORDS    anti-Sm antibody; diversity region; immunoglobulin heavy chain;
            joining region; variable region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 384)
  AUTHORS   Mahmoudi,M., Edwards,J., Cairns,E. and Bell,D.
  TITLE     Molecular characterization of natural human anti-Sm autoantibodies
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 384)
  AUTHORS   Mahmoudi,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (24-OCT-1994) Mahmoudi M., University of Western Ontario,
            Medicine and Microbiology and Immunology, University Hospital Room
            BRE-12, London, Ontario, Canada, N6A 5A5
FEATURES             Location/Qualifiers
     source          1. .384
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                     /db_xref="taxon:9606"
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                     /tissue_type="human tonsil"
     CDS             1. .>384
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                     translation"
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                     /db_xref="GI:1340168"
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     J_segment       325. .384
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ORIGIN

  Query Match             85.4%;  Score 325.4;  DB 9;  Length 384;
  Best Local Similarity   92.4%;  Pred. No. 1.6e-91;
  Matches  354;  Conservative    0;  Mismatches   26;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATA--- 298
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Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATAATT 301

Qy        299 TGGGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAG 358
                  |  |  ||| |  |       ||||||||||||||||||||||||||||||||
Db        302 ATTACTATGATAGTAGTGGTTATTACTACTACTACGGTATGGACGTCTGGGGCCAAG 361

Qy        359 GGACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||||
Db        362 GGACCACGGTCACCGTCTCCTCA 384


RESULT 15
AY607468
LOCUS       AY607468                360 bp    DNA     linear   PRI 03-MAY-2004
DEFINITION  Homo sapiens isolate CB#4/#191/7A immunoglobulin heavy chain CDR3
            gene, partial cds.
ACCESSION   AY607468
VERSION     AY607468.1  GI:46811629
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 360)
  AUTHORS   Sims,G.P.
  TITLE     Developmental regulation of human immunoglobulin heavy chain CDR3
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 360)
  AUTHORS   Sims,G.P.
  TITLE     Direct Submission
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  JOURNAL   Submitted (09-APR-2004) NIAMS Autoimmunity Branch, National
            Institutes of Health, 9000 Rockville Pike, Building 10 Rm 6D44,
            Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1. .360
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                     /tissue_type="term cord blood"
     mRNA            <1. .>360
                     /product="immunoglobulin heavy chain CDR3"
     CDS             <1. .>360
                     /note="rearranged VDJ heavy chain"
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                     /product="immunoglobulin heavy chain CDR3"
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                     YYYGMDVWGQGTTVTVSS"
ORIGIN

  Query Match             85.2%;  Score 324.8;  DB 9;  Length 360;
  Best Local Similarity   93.9%;  Pred. No. 2.5e-91;
  Matches  338;  Conservative    0;  Mismatches   22;  Indels    0;  Gaps    0;

Qy         22 GGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTC 81
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCTCCTGTGCAGCCTCTGGATTC 60

Qy         82 ACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG 141
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTCCAGGCAAGGGGCTGGAGTGG 120

Qy        142 GTGGCAGTTATATCATATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGA 201
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GTGGCAGTTATATCATATGATGGAAGTAATAAATACTATGCAGACTCCGTGAAGGGCCGA 180

Qy        202 TTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA 261
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Db        181 TTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATCTGCAAATGAACAGCCTGAGA 240

Qy        262 GCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGGGGTGGGGCAGTGGCTGGAGA 321
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Db        241 GCTGAGGACACGGCTGTGTATTACTGTGCGAAGTCTGGGGTAGCTGCTACATGGTGGGAT 300

Qy        322 CCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA 381
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Search completed: December  7, 2004, 08:53:03
Job time : 2158.18 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 22:52:33 ; Search time 322.553 Seconds
(without alignments)
6200.629 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
Perfect score: 381
Sequence: 1 gaggtgcagctgctcgagtc.....ccacggtcaccgtctcctca 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
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10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	379.4	99.6	381	2	AAX77236	Aax77236 Human D4.
2	379.4	99.6	414	2	AAV68537	Aav68537 Nucleotid
3	378.4	99.3	1630	3	AAZ50588	Aaz50588 HD70scFv-
4	378.4	99.3	1630	3	AAZ50587	Aaz50587 HD70scFv-
5	324.4	85.1	1413	3	AAA46898	Aaa46898 DNA encod
6	324.4	85.1	1413	10	AAD54349	Aad54349 Human 11.
7	324	85.0	378	12	ADP22221	Adp22221 Human ant
8	324	85.0	382	10	ADK18651	Adk18651 Anti-huma
9	324	85.0	382	12	ADL25435	Adl25435 Human mAb
10	323.2	84.8	372	12	ADP22135	Adp22135 Human ant
11	323.2	84.8	429	3	AAA13939	Aaa13939 Human PTH
12	322.8	84.7	375	12	ADP22315	Adp22315 Human ant
13	322.4	84.6	379	10	ADK18643	Adk18643 Anti-huma
14	322.4	84.6	379	12	ADL25419	Adl25419 Human mAb
15	321.8	84.5	381	4	AAS03436	Aas03436 DNA encod
16	321.6	84.4	429	3	AAA13933	Aaa13933 Human PTH
17	321.6	84.4	429	3	AAA13935	Aaa13935 Human PTH
18	321.6	84.4	429	3	AAA13932	Aaa13932 Human PTH
19	321.2	84.3	375	12	ADP22299	Adp22299 Human ant
20	321.2	84.3	375	12	ADP22311	Adp22311 Human ant
21	320.8	84.2	379	10	ADK18635	Adk18635 Anti-huma
22	320.8	84.2	379	12	ADL25403	Adl25403 Human mAb
23	320.6	84.1	384	12	ADP22159	Adp22159 Human ant
24	320.4	84.1	474	8	ABZ22308	Abz22308 S. pneumo
25	318.4	83.6	429	3	AAA13931	Aaa13931 Human PTH
26	318	83.5	375	12	ADP22167	Adp22167 Human ant
27	318	83.5	375	12	ADP22099	Adp22099 Human ant
28	318	83.5	437	6	ABL53511	Abl53511 Human rec
29	318	83.5	437	6	ABL53512	Abl53512 Human rec
30	318	83.5	487	8	AAD56224	Aad56224 Human AB-
31	318	83.5	7576	8	AAD56208	Aad56208 Human AB-
32	317.6	83.4	366	12	ADP22127	Adp22127 Human ant
33	317.6	83.4	372	9	ADA89237	Ada89237 Human ant
34	316.8	83.1	373	10	ADE28438	Ade28438 Human ant
35	316.8	83.1	429	3	AAA13936	Aaa13936 Human PTH
36	316.4	83.0	375	12	ADP22331	Adp22331 Human ant
37	316.4	83.0	375	12	ADP22163	Adp22163 Human ant
38	316.4	83.0	375	12	ADP22319	Adp22319 Human ant
39	316.4	83.0	375	12	ADP22327	Adp22327 Human ant
40	316.4	83.0	375	12	ADP22323	Adp22323 Human ant
41	316.4	83.0	376	10	ADE28450	Ade28450 Human ant
42	316.4	83.0	376	10	ADE28442	Ade28442 Human ant
43	316.4	83.0	437	6	ABL53510	Abl53510 Human rec
44	316.4	83.0	1413	10	ADE28466	Ade28466 Human ant
45	315.2	82.7	373	10	ADE28488	Ade28488 Human ant

ALIGNMENTS

RESULT 1
AAX77236
ID AAX77236 standard; DNA; 381 BP.
XX
AC AAX77236;
XX
DT 04-AUG-1999 (first entry)
XX
DE Human D4.5 heavy chain variable region encoding DNA.
XX
KW Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW autoimmune disease; scFv-antibody; single-chain Fv; ss.
XX
OS Homo sapiens.
XX
PN WO9925818-A1.
XX
PD 27-MAY-1999.
XX
PF 16-NOV-1998; 98WO-EP007313.
XX
PR 17-NOV-1997; 97EP-00120096.
XX
PA (KUFE/) KUFER P.
XX
PI Kufer P, Raum T, Borschert K, Zettl F, Lutterbuese R;
XX
DR WPI; 1999-338004/28.
DR P-PSDB; AAY17954.
XX
PT Phage display system for identification of binding site domains retaining
PT capacity to bind an epitope.
XX
PS Disclosure; Fig 3.1; 152pp; English.
XX
CC The invention relates to a method of identifying binding site domains
CC (BSD) that retain the capacity of binding to a predetermined epitope when
CC positioned C-terminal of at least one further domain in a recombinant bi-
CC or multivalent polypeptide. The method comprises (a) testing a panel of
CC BSD displayed on the surface of a biological display system as part of a
CC fusion protein for binding to a predetermined epitope, where the fusion
CC protein comprises an additional domain positioned N-terminal of the BSD
CC and an amino acid sequence that mediates anchoring of the fusion protein
CC to the surface of the display system; and (b) identifying a BSD that

```
CC   binds to the predetermined epitope. The method is useful to identify bi-
CC   or multivalent polypeptides that comprise antibody binding sites capable
CC   of efficiently binding to the corresponding antigen. The polypeptides or
CC   antibodies identified by the method are useful therapeutically and
CC   diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC   fragments that bind independently of their position within bifunctional
CC   single-chain fusion proteins can be isolated from combinatorial antibody
CC   libraries using the new in vitro method
XX
SQ.  Sequence 381 BP; 87 A; 93 C; 120 G; 81 T; 0 U; 0 Other;

  Query Match             99.6%;  Score 379.4;  DB 2;  Length 381;
  Best Local Similarity   99.7%;  Pred. No. 1.7e-100;
  Matches  380;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Db        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        361 ACCACGGTCACCGTCTCCTCA 381


RESULT 2
AAV68537
ID   AAV68537 standard; DNA; 414 BP.
XX
AC   AAV68537;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Nucleotide sequence of human D4.5 heavy chain variable region.
XX
KW   Human; D4.5 heavy chain variable region; receptor; antigen; tumour;
KW   auto-immune disease; graft rejection; allergy; inflammatory disease;
KW   endocrine disease; degenerative disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .414
FT                   /*tag=  a
FT                   /product= "human D4.5 heavy chain variable region"
XX
PN   WO9846645-A2.
XX
PD   22-OCT-1998.
XX
PF   14-APR-1998;   98WO-EP002180.
XX
PR   14-APR-1997;   97EP-00106109.
XX
PA   (KUFE/) KUFER P.
PA   (RAUM/) RAUM T.
XX
PI   Kufer P,  Raum T;
XX
DR   WPI; 1998-594564/50.
DR   P-PSDB; AAW80815.
XX
PT   Production of anti-human antigen receptors - by selecting a combination
PT   of functionally rearranged VH and VL immunoglobulin chains expressed from
PT   a recombinant vector.
XX
PS   Claim 9; Fig 7; 84pp; English.
XX
CC   This is the nucleotide sequence of the human D4.5 heavy chain variable
CC   region, used in the method of the invention. for providing receptors that
CC   can be used for targeting antigens in humans without being immunogenic
CC   themselves. Such receptors can be used for treating diseases such as
CC   tumours or auto-immune diseases, graft rejection after transplantation,
CC   infectious diseases by targeting cellular receptors as well as allergic,
CC   inflammatory, endocrine and degenerative diseases by targeting key
CC   molecules involved in the pathological process
XX
SQ   Sequence 414 BP; 93 A; 106 C; 127 G; 88 T; 0 U; 0 Other;

  Query Match             99.6%;  Score 379.4;  DB 2;  Length 414;
  Best Local Similarity   99.7%;  Pred. No. 1.8e-100;
  Matches  380;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Db        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        361 ACCACGGTCACCGTCTCCTCA 381


RESULT 3
AAZ50588
ID   AAZ50588 standard; DNA; 1630 BP.
XX
AC   AAZ50588;
XX
DT   23-MAY-2000  (first entry)
XX
DE   HD70scFv-Ck-interleukin 2 encoding DNA.
XX
KW   HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW   epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
KW   interleukin-2; Ck-domain; kappa light chain constant domain;
KW   heterominibody; multifunctional compound; immunoglobulin; cytostatic;
KW   immunostimulatory; antileukaemia; diagnosis; prevention;
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KW   antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW   leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             39. .1613
FT                   /*tag=  a
FT                   /product= "HD70scFv-Ck-IL-2 chain"
FT   misc_feature    96. .842
FT                   /*tag=  b
FT                   /label= HD70_scFv
XX
PN   WO200006605-A2.
XX
PD   10-FEB-2000.
XX
PF   28-JUL-1999;   99WO-EP005416.
XX
PR   28-JUL-1998;   98EP-00114082.
XX
PA   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI   Kufer P,  Dreier T,  Baeuerle PA,  Borschert K,  Zettl F;
XX
DR   WPI; 2000-195265/17.
DR   P-PSDB; AAY44995.
XX
PT   New multifunctional compounds useful for preventing and/or treating
PT   malignant cell growth and for detection and diagnosis.
XX
PS   Claim 8; Fig 55B; 166pp; English.
XX
CC   The patent discloses heterominibodies which are multifunctional compounds
CC   produceable in a mammalian host cell as a secretable and fully functional
CC   heterodimer of two polypeptide chains, where one of the polypeptide
CC   chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC   heavy chain) and the other chain comprises CL-domain (constant domain of
CC   an immunoglobulin light chain). The polypeptide chains further comprise,
CC   fused to the constant domains at least two (poly)peptides having
CC   different receptor or ligand functions, where further at least two of the
CC   different (poly)peptides lack an intrinsic affinity for one another and
CC   are linked via the constant domains. The heterominibodies have
CC   cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC   activities. These compounds can be used for diagnosing, preventing and
CC   treating malignant cell growth related to malignancies of haematopoietic
CC   cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC   melanomas and sarcomas. The present sequence is a DNA encoding right
CC   chain of a heterominibody comprising HD70 single-chain Fv (scFv) fragment
CC   N-terminally linked to human Ck domain (constant domain of immunoglobulin
CC   -kappa light chain) which bears at its C-terminus the human inflammatory
CC   cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
CC   human epithelial cell adhesion molecule (EpCAM) also called 17-1A antigen
XX
SQ   Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;

  Query Match             99.3%;  Score 378.4;  DB 3;  Length 1630;
  Best Local Similarity   99.7%;  Pred. No. 5.4e-100;
  Matches  379;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
            ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db      462 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 521

Qy       61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
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Db      522 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 581

Qy      121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db      582 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 641

Qy      181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
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Db      642 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 701

Qy      241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
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Db      702 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 761

Qy      301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Db      762 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 821

Qy      361 ACCACGGTCACCGTCTCCTC 380
            ||||||||||||||||||||
Db      822 ACCACGGTCACCGTCTCCTC 841


RESULT 4
AAZ50587
ID   AAZ50587 standard; DNA; 1630 BP.
XX
AC   AAZ50587;
XX
DT   23-MAY-2000  (first entry)
XX
DE   HD70scFv-CH1-GM-CSF chain encoding DNA.
XX
KW   HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW   epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
KW   granulocyte/macrophage colony stimulating factor; heterominibody;
KW   CH1-domain; multifunctional compound; heavy chain constant domain;
KW   immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW   antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW   lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   misc_feature    96. .842
FT                   /*tag=  b
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PN   WO200006605-A2.
XX
PD   10-FEB-2000.
XX
PF   28-JUL-1999;   99WO-EP005416.
XX
PR   28-JUL-1998;   98EP-00114082.
XX
PA   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI   Kufer P,  Dreier T,  Baeuerle PA,  Borschert K,  Zettl F;
XX
DR   WPI; 2000-195265/17.
DR   P-PSDB; AAY44994.
XX
PT   New multifunctional compounds useful for preventing and/or treating
PT   malignant cell growth and for detection and diagnosis.
XX
PS   Claim 8; Fig 55A; 166pp; English.
XX
CC   The patent discloses heterominibodies which are multifunctional compounds
CC   produceable in a mammalian host cell as a secretable and fully functional
CC   heterodimer of two polypeptide chains, where one of the polypeptide
CC   chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC   heavy chain) and the other chain comprises CL-domain (constant domain of
CC   an immunoglobulin light chain). The polypeptide chains further comprise,
CC   fused to the constant domains at least two (poly)peptides having
CC   different receptor or ligand functions, where further at least two of the
CC   different (poly)peptides lack an intrinsic affinity for one another and
```

```
CC   are linked via the constant domains. The heterominibodies have
CC   cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC   activities. These compounds can be used for diagnosing, preventing and
CC   treating malignant cell growth related to malignancies of haematopoietic
CC   cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC   melanomas and sarcomas. The present sequence is a DNA encoding left chain
CC   of a heterominibody comprising HD70 single-chain Fv (scFv) fragment N-
CC   terminally linked to human CH1 domain which bears at its C-terminus the
CC   human inflammatory cytokine granulocyte/macrophage colony stimulating
CC   factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
CC   HD70 scFv specifically recognises the human epithelial cell adhesion
CC   molecule (EpCAM) also called 17-1A antigen
XX
SQ   Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

  Query Match           99.3%;  Score 378.4;  DB 3;  Length 1630;
  Best Local Similarity   99.7%;  Pred. No. 5.4e-100;
  Matches  379;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        462 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 521

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Qy        361 ACCACGGTCACCGTCTCCTC 380
              ||||||||||||||||||||
Db        822 ACCACGGTCACCGTCTCCTC 841


RESULT 5
AAA46898
ID   AAA46898 standard; DNA; 1413 BP.
XX
AC   AAA46898;
XX
DT   03-OCT-2000  (first entry)
XX
DE   DNA encoding the heavy chain of immunoglobulin clone 11.2.1.
XX
KW   Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW   hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW   proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /*tag=  a
XX
PN   WO200037504-A2.
XX
PD   29-JUN-2000.
XX
PF   23-DEC-1999;   99WO-US030895.
XX
PR   23-DEC-1998;   98US-0113647P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Hanson DC,  Neveu MJ,  Mueller EE,  Hanke JH,  Gilman SC,  Davis CG;
PI   Corvalan JR;
XX
DR   WPI; 2000-442647/38.
DR   P-PSDB; AAY93734.
XX
PT   Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT   -4 containing specified heavy and light chain sequences, useful for
PT   treating, e.g. immune disorders.
XX
PS   Example 2; Fig 22p; 157pp; English.
XX
CC   The present sequence encodes a heavy chain of an antibody of the
CC   invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC   -4. Antibodies of the invention are composed of a heavy chain variable
CC   region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC   encoded by a human VH3-33 family gene. The modifications are contained in
CC   CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC   inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC   disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC   proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC   used to up-regulate immune system to up-regulate immunodeficient
CC   disorders
XX
SQ   Sequence 1413 BP; 321 A; 437 C; 395 G; 260 T; 0 U; 0 Other;

  Query Match           85.1%;  Score 324.4;  DB 3;  Length 1413;
  Best Local Similarity   92.9%;  Pred. No. 2.9e-84;
  Matches  353;  Conservative    0;  Mismatches   21;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| ||||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||| ||||  |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGA 358

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || | |  |     |      ||||||||||||||||||||||||||||||||||||
Db        359 GGGGAGCTACCCTTT------ACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 412

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        413 CCACGGTCACCGTCTCCTCA 432


RESULT 6
AAD54349
ID   AAD54349 standard; cDNA; 1413 BP.
XX
AC   AAD54349;
XX
DT   17-JUN-2003  (first entry)
XX
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DE   Human 11.2.1 anti-CTLA-4 antibody heavy chain cDNA.
XX
KW   Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW   cancer; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   sig_peptide     1. .57
FT                   /*tag=  a
FT   mat_peptide     58. .1410
FT                   /*tag=  b
FT                   /product= "Mature anti-CTLA-4 antibody heavy chain"
XX
PN   EP1262193-A1.
XX
PD   04-DEC-2002.
XX
PF   23-MAY-2002; 2002EP-00253652.
XX
PR   23-MAY-2001; 2001US-0293042P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Hanson DC,  Mueller EE;
XX
DR   WPI; 2003-131215/13.
DR   P-PSDB; AAE35889.
XX
PT   Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
PT   preparation of medicament for the treatment of cancer.
XX
PS   Disclosure; Fig 1P; 76pp; English.
XX
CC   The invention relates to the use of human anti-cytotoxic T lymphocyte
CC   antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC   the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC   cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC   cancer, cancer of the anal region, stomach cancer, breast cancer,
CC   testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC   The present sequence is human anti-CTLA-4 antibody heavy chain cDNA
XX
SQ   Sequence 1413 BP; 321 A; 437 C; 395 G; 260 T; 0 U; 0 Other;

  Query Match             85.1%;  Score 324.4;  DB 10;  Length 1413;
  Best Local Similarity   92.9%;  Pred. No. 2.9e-84;
  Matches  353;  Conservative    0;  Mismatches   21;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||| ||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||| ||||  |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGA 358

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || | |  |     |       ||||||||||||||||||||||||||||||||||||
Db        359 GGGGAGCTACCCTTT------ACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 412

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        413 CCACGGTCACCGTCTCCTCA 432
```

```
RESULT 7
ADP22221
ID   ADP22221 standard; cDNA; 378 BP.
XX
AC   ADP22221;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human anti-TNFa antibody light chain variable region cDNA SEQ ID NO:127.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostrate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .378
FT                   /*tag=  a
FT                   /product= "human anti-TNFa antibody light chain variable
FT                   region"
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS,  Kang JS,  Foord O,  Green L,  Feng X,  Klakamp S;
PI   Haak-Frendscho M,  Rathanaswami P,  Pigott C,  Liang ML,  Lee R;
PI   Manchulencho K,  Faggioni R,  Senaldi G,  Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
DR   P-PSDB; ADP22222.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 127; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
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CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence encodes a human anti-TNFa
CC   antibody light chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 378 BP; 85 A; 92 C; 120 G; 81 T; 0 U; 0 Other;

  Query Match             85.0%;  Score 324;  DB 12;  Length 378;
  Best Local Similarity   92.6%;  Pred. No. 2.5e-84;
  Matches  352;  Conservative    0;  Mismatches   25;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||||| |||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||| |||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||||| |||   ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGA---GG 298

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              ||   |    |   |    || ||||||||||||||||||||||||||||||||||||
Db        299 GGATAGCAGTGGCTGGTCCTCCTTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 8
ADK18651
ID   ADK18651 standard; DNA; 382 BP.
XX
AC   ADK18651;
XX
DT   06-MAY-2004  (first entry)
XX
DE   Anti-human PDGF-D antibody heavy chain gene sequence.
XX
KW   ds; gene; antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2003057857-A2.
XX
PD   17-JUL-2003.
XX
PF   06-JAN-2003; 2003WO-US000398.
XX
PR   07-JAN-2002; 2002US-00041860.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Corvalan JRF,  Jia X,  Feng X,  Yang X,  Chen F,  Gazit G,  Weber R;
PI   Bezabeh B;
XX
DR   WPI; 2003-587119/55.
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 75; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a DNA used in the invention.
XX
SQ   Sequence 382 BP; 88 A; 90 C; 118 G; 86 T; 0 U; 0 Other;

  Query Match             85.0%;  Score 324;  DB 10;  Length 382;
  Best Local Similarity   90.8%;  Pred. No. 2.5e-84;
  Matches  345;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||| ||||||||| |||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||| ||||||  |||||||||| | ||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGTATGATGGAAATGATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||| |||||| |||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGCTTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||||||| ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATT 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                |  |  ||| |        | ||||||||||||||||||||||||||||||||||||
Db        302 ACTATGATAGTAGTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        362 CCACGGTCACCGTCTCCTCA 381


RESULT 9
ADL25435
ID   ADL25435 standard; cDNA; 382 BP.
XX
AC   ADL25435;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human mAb 1.38.1 heavy chain variable region encoding cDNA SEQ ID NO:45.
XX
KW   antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW   nephritis; mesangial cell proliferation inhibition;
KW   mesangial proliferative glomerulonephritis; nephrotropic;
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KW   antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW   gene therapy; human; monoclonal antibody; mAb; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .381
FT                   /*tag=  a
FT                   /product= "mAb 1.38.1 heavy chain variable region"
XX
PN   WO2004024098-A2.
XX
PD   25-MAR-2004.
XX
PF   16-SEP-2003; 2003WO-US029414.
XX
PR   16-SEP-2002; 2002US-0411137P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (CURA-) CURAGEN CORP.
XX
PI   Floege J,  Gazit-Bornstein G,  Keyt B,  Larochelle WJ,  Lichenstein H;
XX
DR   WPI; 2004-269881/25.
DR   P-PSDB; ADL25436.
XX
PT   Use of an antibody or its binding fragment that binds platelet derived
PT   growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT   nephritis.
XX
PS   Disclosure; SEQ ID NO 45; 115pp; English.
XX
CC   The present invention describes an antibody or its binding fragment that
CC   binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC   useful in preparing a medicament for treating nephritis. Also described:
CC   (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC   (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC   of treating mesangial proliferative glomerulonephritis. The antibody has
CC   nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC   antidiabetic activities, and can be used in gene therapy. The antibody or
CC   its binding fragment, that binds PDGF-DD, can be used in preparing a
CC   medicament for treating nephritis and related disorders, e.g., mesangial
CC   proliferative glomerulonephritis. The present sequence encodes a human
CC   monoclonal antibody (mAb) variable region sequence, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 382 BP; 88 A; 90 C; 118 G; 86 T; 0 U; 0 Other;

  Query Match             85.0%;  Score 324;  DB 12;  Length 382;
  Best Local Similarity   90.8%;  Pred. No. 2.5e-84;
  Matches  345;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||| |||||||||| |||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||| ||||||  |||||||||| | ||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGTATGATGGAAATGATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGCTTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATT 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              |  |  ||| |       | ||||||||||||||||||||||||||||||||||||
Db        302 ACTATGATAGTAGTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        362 CCACGGTCACCGTCTCCTCA 381


RESULT 10
ADP22135
ID   ADP22135 standard; cDNA; 372 BP.
XX
AC   ADP22135;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human anti-TNFa antibody heavy chain variable region cDNA SEQ ID NO:41.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostrate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .372
FT                   /*tag=  a
FT                   /product= "human anti-TNFa antibody heavy chain variable
FT                   region"
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS,  Kang JS,  Foord O,  Green L,  Feng X,  Klakamp S;
PI   Haak-Frendscho M,  Rathanaswami P,  Pigott C,  Liang ML,  Lee R;
PI   Manchulencho K,  Faggioni R,  Senaldi G,  Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
DR   P-PSDB; ADP22136.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 41; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
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CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence encodes a human anti-TNFa
CC   antibody heavy chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 372 BP; 85 A; 89 C; 115 G; 83 T; 0 U; 0 Other;

  Query Match             84.8%;  Score 323.2;  DB 12;  Length 372;
  Best Local Similarity   92.9%;  Pred. No. 4.2e-84;
  Matches  353;  Conservative    0;  Mismatches   18;  Indels    9;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||| || | ||||||||||||||| |||||||||||||||||||||||||||||
Db          2 AGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTATTAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||  |||||||||||||||||||||||||||||||||||||||||||||||  |||
Db        242 TGCAAGTGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGA----- 296

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                  || | || |  ||||   |||||| |||||| ||||||||||||||||||||||||
Db        297 ----GGTCCGTAGTGGGAGCTACTACTATTACTACAGTATGGACGTCTGGGGCCAAGGGA 352

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        353 CCACGGTCACCGTCTCCTCA 372


RESULT 11
AAA13939
ID   AAA13939 standard; DNA; 429 BP.
XX
AC   AAA13939;
XX
DT   02-AUG-2000  (first entry)
XX
DE   Human PTHrP monoclonal antibody clone 5B12-16-12 DNA SEQ ID NO:41.
XX
KW   Human; parathyroid hormone related protein; PTHrP; monoclonal antibody;
KW   hypercalcaemia; rheumatoid arthritis; bone cancer; metastasis; pain;
KW   fracture; cachexia; tooth disease; periodontal disease; gingiva; sepsis;
KW   systemic inflammatory response syndrome; SIRS; hypophosphataemia;
KW   antiarthritic; cytostatic; antiinflammatory; ds.
XX
OS   Homo sapiens.
XX
PN   JP2000080100-A.
XX
PD   21-MAR-2000.
XX
PF   12-OCT-1998;   98JP-00304793.
XX
PR   17-JUN-1998;   98JP-00188196.
PR   26-JUN-1998;   98JP-00196729.
XX
PA   (NISB ) JAPAN TOBACCO INC.
XX
DR   WPI; 2000-286723/25.
DR   P-PSDB; AAY82629.
XX
PT   A human monoclonal antibody to parathyroid hormone related protein. -
PT   useful for treating hypercalcemia, rheumatoid arthritis, cancer of bone
PT   including metastasis, and pain.
XX
PS   Example 10; Page 76; 88pp; Japanese.
XX
CC   The present invention describes a human monoclonal antibody to
CC   parathyroid hormone related protein (PTHrP). The monoclonal antibody or
CC   its fragments, following the stimulation of PTHrP has the following
CC   properties: (a) inhibits intracellular elevation of cAMP; (b) inhibits
CC   the release of calcium from bone; or (c) inhibits elevation of blood
CC   calcium content. The monoclonal antibody can be used in the treatment of
CC   hypercalcaemia, rheumatoid arthritis, cancer of bone including
CC   metastasis, pain, fracture, cachexia, diseases of teeth, periodontal
CC   diseases and gingiva, sepsis, systemic inflammatory response syndrome
CC   (SIRS) and hypophosphataemia. It has antiarthritic, cytostatic and
CC   antiinflammatory activities. The present sequence represents a human
CC   PTHrP monoclonal antibody clone nucleotide sequence from the present
CC   invention
XX
SQ   Sequence 429 BP; 92 A; 99 C; 138 G; 100 T; 0 U; 0 Other;

  Query Match             84.8%;  Score 323.2;  DB 3;  Length 429;
  Best Local Similarity   92.9%;  Pred. No. 4.4e-84;
  Matches  353;  Conservative    0;  Mismatches   18;  Indels    9;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||||| |||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 TAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||||||||||||||||||||||||||||||| | | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGACACA--- 355

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                  ||||||||||        ||||||||||||||||||||||||||||||||||||
Db        356 ------GCAGTGGCTGGTACGAGGACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 409

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        410 CCACGGTCACCGTCTCCTCA 429


RESULT 12
ADP22315
ID   ADP22315 standard; cDNA; 375 BP.
```

XX
AC ADP22315;
XX
DT 09-SEP-2004 (first entry)
XX
DE Human anti-TNFa antibody heavy chain variable region cDNA SEQ ID NO:221.
XX
KW human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW prostrate cancer; immuno-mediated inflammatory disease;
KW rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW septic shock; cachexia; anorexia; multiple sclerosis; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .375
FT /*tag= a
FT /product= "human anti-TNFa antibody heavy chain variable
FT region"
XX
PN WO2004050683-A2.
XX
PD 17-JUN-2004.
XX
PF 02-DEC-2003; 2003WO-US038281.
XX
PR 02-DEC-2002; 2002US-0430729P.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Babcook JS, Kang JS, Foord O, Green L, Feng X, Klakamp S;
PI Haak-Frendscho M, Rathanaswami P, Pigott C, Liang ML, Lee R;
PI Manchulencho K, Faggioni R, Senaldi G, Qiaojuan JS;
XX
DR WPI; 2004-480601/45.
DR P-PSDB; ADP22316.
XX
PT New recombinant human monoclonal antibody that specifically binds to
PT Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT arthritis.
XX
PS Example 10; SEQ ID NO 221; 213pp; English.
XX
CC The present invention describes a human monoclonal antibody (I) that
CC specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC (M1) the level of TNFa in a patient sample, comprising contacting with
CC (I), and detecting the level of binding between the antibody and TNFa in
CC the sample; (2) a composition comprising the antibody or its functional
CC fragment and a carrier; (3) treating (M2) an animal suffering from a
CC neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC animal in need of treatment for the disease by administering the human
CC monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC apoptosis in an animal by selecting an animal in need of treatment for
CC TNFa induced apoptosis by administering the human monoclonal antibody of
CC (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC disorders, immunomodulator, immunosuppressive, nephrotropic,
CC neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC medicament for treating TNF induced apoptosis, neoplastic disease such as
CC breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC diseases such as rheumatoid arthritis, glomerulonephritis,
CC atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC multiple sclerosis. The present sequence encodes a human anti-TNFa
CC antibody heavy chain variable region, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 375 BP; 87 A; 92 C; 116 G; 80 T; 0 U; 0 Other;

Query Match 84.7%; Score 322.8; DB 12; Length 375;
Best Local Similarity 92.6%; Pred. No. 5.5e-84;
Matches 352; Conservative 0; Mismatches 22; Indels 6; Gaps 1;

```
Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||||| ||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGACATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||| |||||||||||||||||| ||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATATCATATGATGGAAGTATTAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||| |  |
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGAGAATG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |    ||  |     ||||||| |||||||||||||||||||||||||||||||||
Db        302 CGGTGACTTACGGGGG------CTACTACCACTACGGTATGGACGTCTGGGGCCAAGGGA 355

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        356 CCACGGTCACCGTCTCCTCA 375
```

RESULT 13
ADK18643
ID ADK18643 standard; DNA; 379 BP.
XX
AC ADK18643;
XX
DT 06-MAY-2004 (first entry)
XX
DE Anti-human PDGF-D antibody heavy chain gene sequence.
XX
KW ds; gene; antiinflammatory; immunomodulator; cytostatic; gene therapy.
XX
OS Homo sapiens.
XX
PN WO2003057857-A2.
XX
PD 17-JUL-2003.
XX
PF 06-JAN-2003; 2003WO-US000398.
XX
PR 07-JAN-2002; 2002US-00041860.
XX
PA (ABGE-) ABGENIX INC.
XX
PI Corvalan JRF, Jia X, Feng X, Yang X, Chen F, Gazit G, Weber R;
PI Bezabeh B;
XX
DR WPI; 2003-587119/55.

```
XX
PT   New human monoclonal antibody that binds to platelet-derived growth
PT   factor-D (PDGF-D), useful for treating chronic and recurrent human
PT   diseases, such as inflammation, autoimmunity and cancer.
XX
PS   Disclosure; SEQ ID NO 67; 255pp; English.
XX
CC   The invention relates to a human monoclonal antibody that binds to
CC   platelet-derived growth factor-D (PDGF-D). The antibodies are useful for
CC   treating chronic and recurrent human diseases, such as inflammation,
CC   autoimmunity and cancer. The PDGF-D nucleic acids and polypeptides are
CC   useful for modulating collagen formation, and for staging various
CC   cancers. Antibodies to platelet-derived growth factor-D (PDGF-D) were
CC   generated using an active protein fragment of the gene product from the
CC   clone 30664188.0.99 arising in the conditioned medium obtained when
CC   HEK293 cells are transfected with the plasmid pCEP4/Sec-30664188. This
CC   sequence corresponds to a DNA used in the invention.
XX
SQ   Sequence 379 BP; 88 A; 88 C; 121 G; 82 T; 0 U; 0 Other;

  Query Match             84.6%;  Score 322.4;  DB 10;  Length 379;
  Best Local Similarity   92.4%;  Pred. No. 7.2e-84;
  Matches  351;  Conservative    0;  Mismatches   26;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||  ||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCAGTTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||| ||||||| ||||  ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |   ||  ||| |       ||||||| |||||||||||||||||||||||||||||||
Db        302 GATACAGCTATGGTT---ACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 14
ADL25419
ID   ADL25419 standard; cDNA; 379 BP.
XX
AC   ADL25419;
XX
DT   17-JUN-2004  (first entry)
XX
DE   Human mAb 1.24.1 heavy chain variable region encoding cDNA SEQ ID NO:29.
XX
KW   antibody; binding fragment; platelet derived growth factor-DD; PDGF-DD;
KW   nephritis; mesangial cell proliferation inhibition;
KW   mesangial proliferative glomerulonephritis; nephrotropic;
KW   antiinflammatory; dermatological; immunosuppressive; antidiabetic;
KW   gene therapy; human; monoclonal antibody; mAb; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .378
FT                   /*tag=  a
FT                   /product= "mAb 1.24.1 heavy chain variable region"
XX
PN   WO2004024098-A2.
XX
PD   25-MAR-2004.
XX
PF   16-SEP-2003; 2003WO-US029414.
XX
PR   16-SEP-2002; 2002US-0411137P.
XX
PA   (ABGE-) ABGENIX INC.
PA   (CURA-) CURAGEN CORP.
XX
PI   Floege J,  Gazit-Bornstein G,  Keyt B,  Larochelle WJ,  Lichenstein H;
XX
DR   WPI; 2004-269881/25.
DR   P-PSDB; ADL25420.
XX
PT   Use of an antibody or its binding fragment that binds platelet derived
PT   growth factor-DD (PDGF-DD) for preparing a medicament for treating
PT   nephritis.
XX
PS   Disclosure; SEQ ID NO 29; 115pp; English.
XX
CC   The present invention describes an antibody or its binding fragment that
CC   binds platelet derived growth factor-DD (PDGF-DD), where the antibody is
CC   useful in preparing a medicament for treating nephritis. Also described:
CC   (1) a method of detecting nephritis; (2) a method of treating nephritis;
CC   (3) a method of inhibiting mesangial cell proliferation; and (4) a method
CC   of treating mesangial proliferative glomerulonephritis. The antibody has
CC   nephrotropic, antiinflammatory, dermatological, immunosuppressive and
CC   antidiabetic activities, and can be used in gene therapy. The antibody or
CC   its binding fragment, that binds PDGF-DD, can be used in preparing a
CC   medicament for treating nephritis and related disorders, e.g., mesangial
CC   proliferative glomerulonephritis. The present sequence encodes a human
CC   monoclonal antibody (mAb) variable region sequence, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 379 BP; 88 A; 88 C; 121 G; 82 T; 0 U; 0 Other;

  Query Match             84.6%;  Score 322.4;  DB 12;  Length 379;
  Best Local Similarity   92.4%;  Pred. No. 7.2e-84;
  Matches  351;  Conservative    0;  Mismatches   26;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||  ||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCAGTTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||| ||||||| ||||  ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |   ||  ||| |       ||||||| |||||||||||||||||||||||||||||||
Db        302 GATACAGCTATGGTT---ACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378
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RESULT 15
AAS03436
ID   AAS03436 standard; cDNA; 381 BP.
XX
AC   AAS03436;
XX
DT   29-AUG-2001  (first entry)
XX
DE   DNA encoding anti-adipocyte monoclonal antibody heavy chain, FAT 25.
XX
KW   Antibody; adipocyte; heavy chain; light chain; obesity; FAT;
KW   heart disease; complementarity determining region; CDR; ss.
XX
OS   Homo sapiens.
XX
PN   WO200127279-A1.
XX
PD   19-APR-2001.
XX
PF   11-OCT-2000; 2000WO-GB003900.
XX
PR   12-OCT-1999;   99US-0158812P.
XX
PA   (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
PI   Edwards BM,  Main SH,  Vaughan TJ;
XX
DR   WPI; 2001-282031/29.
DR   P-PSDB; AAU02536.
XX
PT   Panel of specific binding members of antibody molecules which bind to
PT   whole adipocytes is used in the treatment of obesity and obesity related
PT   diseases.
XX
PS   Disclosure; Page 114; 182pp; English.
XX
CC   AAS03401-AAS03535 represent anti-adipocyte monoclonal antibody heavy and
CC   light chain coding sequences of the invention. The antibodies can be used
CC   in the treatment of obesity and obesity related diseases. The antibodies
CC   can be used to deliver drugs or pro-drugs directly to the fat mass of an
CC   obese patient or the antibody can be used as a therapeutic itself.
CC   Antibodies binding specifically to adipocytes can be used to activate the
CC   immune system to destroy the cells by complement mediated lysis. The
CC   antibodies may be labeled with a detectable label such as radiolabel,
CC   fluorescent or chemical group and used in methods of diagnosis in human
CC   subjects e.g. to determine the presence of adipocyte antigen on the
CC   surface of an adipocyte to detect or determine the presence or level of
CC   adipocytes in a cell or tissue sample. The antibodies can be used as an
CC   alternative means of treatment for obese patients other than undergoing
CC   surgery to remove excess fat. Antibodies for different types of fat
CC   deposits can also be produced e.g. intra- abdominal fat associated with
CC   heart disease
XX
SQ   Sequence 381 BP; 87 A; 89 C; 122 G; 83 T; 0 U; 0 Other;

  Query Match             84.5%;  Score 321.8;  DB 4;  Length 381;
  Best Local Similarity   90.3%;  Pred. No. 1.1e-83;
  Matches  344;  Conservative    0;  Mismatches   37;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              ||||||||||| | ||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              |||||||||||||||||||||||||| | ||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGGAACTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTGATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGGAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              |||||||||||||||||||||||| ||||||||||||| |||||||||||| |      |
Db        241 CTGCAAATGAACAGCCTGAGAGTCGAGGACACGGCTGTTTATTACTGTGCGAGAAGATGG 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              | ||||||||| |   |   | ||| ||||| |   ||||||| ||||||| |||||
Db        301 TATGGTGGCAGTGGTTATTGGGGCCACTTCTACTCCTACATGGACGGCTGGGGCAAAGGG 360

Qy        361 ACCACGGTCACCGTCTCCTCA 381
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Search completed: December  7, 2004, 06:41:26
Job time : 324.553 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 05:42:24 ; Search time 78.6581 Seconds
(without alignments)
3442.884 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
Perfect score: 381
Sequence: 1 gaggtgcagctgctcgagtc.....ccacggtcaccgtctcctca 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	324.4	85.1	1413	4	US-09-472-087-61	Sequence 61, Appl
	2	313.8	82.4	378	3	US-09-240-274-95	Sequence 95, Appl
	3	310.6	81.5	378	3	US-09-240-274-94	Sequence 94, Appl
	4	310.6	81.5	378	3	US-09-240-274-196	Sequence 196, App
	5	308.8	81.0	372	4	US-09-424-840-15	Sequence 15, Appl
	6	307.6	80.7	369	4	US-09-424-840-5	Sequence 5, Appli
	7	304.2	79.8	378	3	US-09-240-274-195	Sequence 195, App
	8	301	79.0	378	3	US-09-240-274-189	Sequence 189, App
	9	300.4	78.8	867	3	US-08-862-124-16	Sequence 16, Appl
	10	300.4	78.8	918	3	US-08-862-124-13	Sequence 13, Appl
c	11	300.4	78.8	918	3	US-08-862-124-15	Sequence 15, Appl
	12	299.6	78.6	369	4	US-09-560-198A-1	Sequence 1, Appli
	13	299.4	78.6	381	3	US-09-240-274-87	Sequence 87, Appl
c	14	298.8	78.4	867	3	US-08-862-124-18	Sequence 18, Appl
	15	297.8	78.2	378	3	US-09-240-274-86	Sequence 86, Appl
	16	296.4	77.8	503	4	US-09-472-087-35	Sequence 35, Appl
	17	296.2	77.7	381	3	US-09-240-274-88	Sequence 88, Appl
	18	295.8	77.6	512	3	US-08-545-809A-30	Sequence 30, Appl
	19	294.2	77.2	369	4	US-09-560-198A-3	Sequence 3, Appli
	20	293.2	77.0	369	4	US-09-560-198A-9	Sequence 9, Appli
	21	291.4	76.5	381	3	US-09-240-274-182	Sequence 182, App
	22	289.8	76.1	378	3	US-09-240-274-84	Sequence 84, Appl
	23	289.8	76.1	378	3	US-09-240-274-85	Sequence 85, Appl
	24	288.6	75.7	375	3	US-09-240-274-183	Sequence 183, App
	25	288.2	75.6	378	3	US-09-240-274-83	Sequence 83, Appl
	26	287.2	75.4	562	4	US-09-472-087-38	Sequence 38, Appl
	27	287	75.3	372	3	US-09-240-274-73	Sequence 73, Appl
	28	286.6	75.2	378	3	US-09-240-274-190	Sequence 190, App
	29	285.8	75.0	372	3	US-09-240-274-74	Sequence 74, Appl
	30	285.4	74.9	375	3	US-09-240-274-89	Sequence 89, Appl
	31	285	74.8	378	3	US-09-240-274-79	Sequence 79, Appl
	32	285	74.8	378	3	US-09-240-274-187	Sequence 187, App
	33	285	74.8	381	3	US-09-240-274-188	Sequence 188, App
	34	284.8	74.8	384	3	US-09-240-274-70	Sequence 70, Appl
	35	284.4	74.6	342	2	US-08-477-553A-53	Sequence 53, Appl
	36	284.2	74.6	372	3	US-09-240-274-71	Sequence 71, Appl
	37	284.2	74.6	372	3	US-09-240-274-75	Sequence 75, Appl
	38	283.8	74.5	375	3	US-09-240-274-90	Sequence 90, Appl
	39	283.4	74.4	378	3	US-09-240-274-193	Sequence 193, App
	40	283.2	74.3	384	3	US-09-240-274-185	Sequence 185, App
	41	282.8	74.2	375	3	US-09-240-274-91	Sequence 91, Appl
	42	282.6	74.2	372	3	US-09-240-274-76	Sequence 76, Appl
	43	282.2	74.1	375	3	US-09-240-274-77	Sequence 77, Appl
	44	281.4	73.9	583	3	US-08-545-809A-33	Sequence 33, Appl
	45	280.8	73.7	933	3	US-09-079-029-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1
US-09-472-087-61
; Sequence 61, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
; APPLICANT: HANSON, DOUGLAS C.
; APPLICANT: NEVEU, MARK J.
; APPLICANT: MUELLER, EILLEN E.
; APPLICANT: HANKE, JEFFREY H.
; APPLICANT: GILMAN, STEVEN C.
; APPLICANT: DAVIS, C. GEOFFREY
; APPLICANT: CORVALAN, JOSE R.
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
; FILE REFERENCE: ABX-PF1
; CURRENT APPLICATION NUMBER: US/09/472,087
; CURRENT FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/113,647
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 147
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
; LENGTH: 1413
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-472-087-61

Query Match 85.1%; Score 324.4; DB 4; Length 1413;
Best Local Similarity 92.9%; Pred. No. 3e-93;
Matches 353; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||||| |||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||| |||||||||||||||||||||||||| ||||  |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGA 358
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Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || | |  |    |  .  ||||||||||||||||||||||||||||||||||||||||
Db        359 GGGGAGCTACCCTTT------ACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 412

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        413 CCACGGTCACCGTCTCCTCA 432


RESULT 2
US-09-240-274-95
; Sequence 95, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 95
;   LENGTH: 378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D31
US-09-240-274-95

  Query Match             82.4%;  Score 313.8;  DB 3;  Length 378;
  Best Local Similarity   90.8%;  Pred. No. 3.9e-90;
  Matches  346;  Conservative    0;  Mismatches   32;  Indels    3;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 TCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGGCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||||||||| | |  ||||||||||||| ||| |||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTGTCTACTATGATGGAAGTAACAAACACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        181 TCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              || |||||| ||||||||||||| ||||||||||||||||||||||||||||| ||| |
Db        241 CTACAAATGGACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAAGA 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
                |   | ||||| |      ||  ||||||||||||||||||||||||||||| ||||
Db        301 AATTTTCGGAGTGGTT---ATTCCCGCTACTACTACGGTATGGACGTCTGGGGCCCAGGG 357

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        358 ACCACGGTCACCGTCTCCTCA 378


RESULT 3
US-09-240-274-94
; Sequence 94, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 94
;   LENGTH: 378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D30
US-09-240-274-94

  Query Match             81.5%;  Score 310.6;  DB 3;  Length 378;
  Best Local Similarity   90.3%;  Pred. No. 4.1e-89;
  Matches  344;  Conservative    0;  Mismatches   34;  Indels    3;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              |||||||||||| ||||||||||||||||||||||||||||| ||||||||| ||||||
Db         61 TCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCGCTGGGTCCGGCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||||||||| | |  ||||||||||||| ||| |||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTGTCTACTATGATGGAAGTAACAAACACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db        181 TCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAACTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              || |||||| ||||||||||||| ||||||||||||||||||||||||||||| ||| |
Db        241 CTACAAATGGACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAAGA 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
                |   | ||||| |      ||  ||||||||||||||||||||||||||||| ||||
Db        301 AATTTTCGGAGTGGTT---ATTCCCGCTACTACTACGGTATGGACGTCTGGGGCCCAGGG 357

Qy        361 ACCACGGTCACCGTCTCCTCA 381
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Db        358 ACCACGGTCACCGTCTCCTCA 378


RESULT 4
US-09-240-274-196
; Sequence 196, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 196
;   LENGTH: 378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
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;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH56
US-09-240-274-196

  Query Match             81.5%;  Score 310.6;  DB 3;  Length 378;
  Best Local Similarity   90.3%;  Pred. No. 4.1e-89;
  Matches  344;  Conservative    0;  Mismatches   34;  Indels    3;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||| ||||||||| |||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              |||||||||| |||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 TCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGGCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||||||| | |  ||||||||||||| ||| |||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTGTCTACTATGATGGAAGTAACAAACACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||
Db        181 TCAGACTCCGTGAAGGGCCGATTCACCATCTTCAGAGACAACTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              || |||||| |||||||||||| |||||||||||||||||||||||||| ||| |
Db        241 CTACAAATGGACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGAAAGA 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              |   | ||||| |      ||  |||||||||||||||||||||||||| ||||
Db        301 AATTTTCGGAGTGGTT---ATTCCCGCTACTACTACGGTATGGACGTCTGGGGCCCAGGG 357

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        358 ACCACGGTCACCGTCTCCTCA 378


RESULT 5
US-09-424-840-15
; Sequence 15, Application US/09424840
; Patent No. 6790938
; GENERAL INFORMATION:
;  APPLICANT:  BERCHTOLD, Peter
;  APPLICANT:  ESCHER, Robert F.A.
;  TITLE OF INVENTION:  Anti-GPIIB/IIIA Recombinant Antibodies
;  FILE REFERENCE:  100564-09049
;  CURRENT APPLICATION NUMBER: US/09/424,840
;  CURRENT FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER:  DE 19723904.8
;  PRIOR FILING DATE:  1997-06-06
;  PRIOR APPLICATION NUMBER:  DE 19755227.7
;  PRIOR FILING DATE:  1997-12-12
;  PRIOR APPLICATION NUMBER:  DE 19820663.1
;  PRIOR FILING DATE:  1998-05-08
;  NUMBER OF SEQ ID NOS:  127
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 15
;   LENGTH: 372
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(372)
US-09-424-840-15

  Query Match             81.0%;  Score 308.8;  DB 4;  Length 372;
  Best Local Similarity   90.5%;  Pred. No. 1.5e-88;
  Matches  344;  Conservative    0;  Mismatches   27;  Indels    9;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||  | |||||||||||||||||| ||||||| ||||||||||||||||||||||
Db          2 AGGTGAAACTGCTCGAGTCTGGGGGAGGCGTGGTCCACCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATACTATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||| |||||||||||||||||||| |||||||||| |
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCACTTATATCATATGATGGAAGCAATAAATACTACG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db        182 CAGACTCCGTGAAGGGCCGATTCGCCATCTCCAGAGACAATTCCAAGAACACGCTATATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---- 297

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                  ||| |  |  ||||   |  |   | | |||||||||||||||||||||||||||
Db        298 -----GGCCGGAGTGGGAGCTACGCCAGGTTCGACGGTATGGACGTCTGGGGCCAAGGGA 352

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        353 CCACGGTCACCGTCTCCTCA 372


RESULT 6
US-09-424-840-5
; Sequence 5, Application US/09424840
; Patent No. 6790938
; GENERAL INFORMATION:
;  APPLICANT:  BERCHTOLD, Peter
;  APPLICANT:  ESCHER, Robert F.A.
;  TITLE OF INVENTION:  Anti-GPIIB/IIIA Recombinant Antibodies
;  FILE REFERENCE:  100564-09049
;  CURRENT APPLICATION NUMBER: US/09/424,840
;  CURRENT FILING DATE:  1999-12-03
;  PRIOR APPLICATION NUMBER:  DE 19723904.8
;  PRIOR FILING DATE:  1997-06-06
;  PRIOR APPLICATION NUMBER:  DE 19755227.7
;  PRIOR FILING DATE:  1997-12-12
;  PRIOR APPLICATION NUMBER:  DE 19820663.1
;  PRIOR FILING DATE:  1998-05-08
;  NUMBER OF SEQ ID NOS:  127
;  SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 5
;   LENGTH: 369
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(369)
US-09-424-840-5

  Query Match             80.7%;  Score 307.6;  DB 4;  Length 369;
  Best Local Similarity   90.5%;  Pred. No. 3.6e-88;
  Matches  344;  Conservative    0;  Mismatches   24;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||  | |||||||||||||||||| ||||||| ||||||||||||||||||||||
Db          2 AGGTGAAACTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||||   ||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||| |
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAATAAATACTACG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||
Db        182 CAGACTCCGTGAAGGGCCGATTCGCCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
```

```
Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||   |||
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGCGCTGG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || |  |  | || |||   | ||||           |||||||||||||||| ||||||
Db        302 GGAGCTGGGGGGGTTGGGACCACTAC----------ATGGACGTCTGGGGCAAAGGGA 349

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        350 CCACGGTCACCGTCTCCTCA 369


RESULT 7
US-09-240-274-195
; Sequence 195, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 195
;   LENGTH: 378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH54
US-09-240-274-195

  Query Match             79.8%;  Score 304.2;  DB 3;  Length 378;
  Best Local Similarity   89.2%;  Pred. No. 4.4e-87;
  Matches  340;  Conservative    0;  Mismatches   38;  Indels    3;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCGGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              |||||||||| ||||| |||||||||||||  ||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCGTCTGGGTTCACCTTCAGTAGGAATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              || |||||||||||||||||||||||| ||||||  | ||||||||||||||||||||||
Db        121 CCTGGCAAGGGGCTGGAGTGGGTGGCATTTATATGGTTTGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              |||||||||||||||||||||||| || |||||||||||||||||||||||||||||    |
Db        241 CTGCAAATGAACAGCCTGAGAGCCGACGACACGGCTGTGTATTACTGTGCGAGAGAGGAG 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              |    |    | ||    |   |    | ||||||||||||||||||||||||||||||
Db        301 GCTCTGTTTCGGGGACTTA---CTCGGTGGTCCTACGGTATGGACGTCTGGGGCCAAGGG 357

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||| ||||||||||
Db        358 ACCACGGTCAGCGTCTCCTCA 378


RESULT 8
US-09-240-274-189
; Sequence 189, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 189
;   LENGTH: 378
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH28, SH50, and SH53
US-09-240-274-189

  Query Match             79.0%;  Score 301;  DB 3;  Length 378;
  Best Local Similarity   88.7%;  Pred. No. 4.6e-86;
  Matches  338;  Conservative    0;  Mismatches   40;  Indels    3;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||| |||||
Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGGGGTCCAGCCTGGGAGGTCCCTGCGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              |||||||| || |||||||||||||||| ||| |||| |||| ||||||||||||||| ||
Db         61 TCCTGTGCGGCGTCTGGATTCACCTTCAATAGTTATGCCATGTACTGGGTCCGCCAGCCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||||||||| |||||  |||||||||||||||||| | |||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAATAAAGAATAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              |||||  |  |||||||||||||||||||||||||||||||||||||||||||||||| |
Db        181 GCAGATTTTGTGAAGGGCCGCTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTCT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              |||||||||||||||||||||||  |||||||||||||||||||||||||||||| |||   |
Db        241 CTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCGAGAGAGGCG 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
                  | ||||||||     |     ||||||||||||||||||||||||||||||||||||
Db        301 AATCTCCTCCGTGGCTGG---TCTCGATACTACTACGGTATGGACGTCTGGGGCCAAGGG 357

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||
Db        358 ACCACGGTCACCGTCTCCTCA 378


RESULT 9
US-08-862-124-16
; Sequence 16, Application US/08862124
; Patent No. 6207153
;  GENERAL INFORMATION:
;    APPLICANT:  Dan, Michael D.
;    APPLICANT:  Maiti, Pradip K.
;    APPLICANT:  Kaplan, Howard A.
;    TITLE OF INVENTION:  ANTIGEN BINDING FRAGMENTS H11, THAT
;    TITLE OF INVENTION:  SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;    TITLE OF INVENTION:  FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;    TITLE OF INVENTION:  DETECTION OF CANCERS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster LLP
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
```

```
;       STATE:  CA
;       COUNTRY:  USA
;       ZIP:  94304-1018
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/862,124
;       FILING DATE:  22-MAY-1997
;       CLASSIFICATION:  424
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Lehnhardt, Susan K.
;       REGISTRATION NUMBER:  33,943
;       REFERENCE/DOCKET NUMBER:  31608-20001.20
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (650) 813-5600
;       TELEFAX:  (650) 494-0792
;       TELEX:  706141
;   INFORMATION FOR SEQ ID NO:  16:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  867 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  join(1..855, 862..867)
US-08-862-124-16

  Query Match             78.8%;  Score 300.4;  DB 3;  Length 867;
  Best Local Similarity   88.9%;  Pred. No. 1e-85;
  Matches  338;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||||| ||||||||||||||||||||||||||||||
Db        428 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 487

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||| ||||||| |||| ||  ||||||||||||||||||||||
Db        488 CCTGTGCAGCCTCTGGATTCCCCTTCAGAAGCTTTGCTATGCACTGGGTCCGCCAGGCTC 547

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||| |
Db        548 TAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCACTAAATACTACG 607

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Db        608 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGGTGTATC 667

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              | |||||||||||||||| |||||||||||||| |||||||||||||| ||||  |
Db        668 TAAAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGAGATCAGA 727

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              |  |   ||| ||       || |||||||||| |||||||||||||| ||||||
Db        728 GCCTGTTGGGTGACT------ATGACCACTACTACGGTTTGGACGTCTGGGGCAAAGGGA 781

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        782 CCACGGTCACCGTCTCCTCA 801


RESULT 10
US-08-862-124-13
; Sequence 13, Application US/08862124
; Patent No. 6207153
;  GENERAL INFORMATION:
;    APPLICANT:  Dan, Michael D.
;    APPLICANT:  Maiti, Pradip K.
;    APPLICANT:  Kaplan, Howard A.
;    TITLE OF INVENTION:  ANTIGEN BINDING FRAGMENTS H11, THAT
;    TITLE OF INVENTION:  SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;    TITLE OF INVENTION:  FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;    TITLE OF INVENTION:  DETECTION OF CANCERS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster LLP
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,124
;      FILING DATE:  22-MAY-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lehnhardt, Susan K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  31608-20001.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  918 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  join(1..906, 913..918)
US-08-862-124-13

  Query Match             78.8%;  Score 300.4;  DB 3;  Length 918;
  Best Local Similarity   88.9%;  Pred. No. 1.1e-85;
  Matches  338;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||||| ||||||||||||||||||||||||||||||
Db        479 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 538

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||| ||||||| |||| ||  ||||||||||||||||||||||
Db        539 CCTGTGCAGCCTCTGGATTCCCCTTCAGAAGCTTTGCTATGCACTGGGTCCGCCAGGCTC 598

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||| |
Db        599 TAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCACTAAATACTACG 658

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||| |||||||||||||| ||||||
Db        659 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGGTGTATC 718

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              | |||||||||||||||| |||||||||||||| |||||||||||||| ||||  |
Db        719 TAAAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGAGATCAGA 778

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              |  |   ||| ||       || |||||||||| |||||||||||||| ||||||
Db        779 GCCTGTTGGGTGACT------ATGACCACTACTACGGTTTGGACGTCTGGGGCAAAGGGA 832

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        833 CCACGGTCACCGTCTCCTCA 852


RESULT 11
```

```
US-08-862-124-15/c
; Sequence 15, Application US/08862124
; Patent No. 6207153
;  GENERAL INFORMATION:
;    APPLICANT:  Dan, Michael D.
;    APPLICANT:  Maiti, Pradip K.
;    APPLICANT:  Kaplan, Howard A.
;    TITLE OF INVENTION:  ANTIGEN BINDING FRAGMENTS H11, THAT
;    TITLE OF INVENTION:  SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;    TITLE OF INVENTION:  FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;    TITLE OF INVENTION:  DETECTION OF CANCERS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster LLP
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,124
;      FILING DATE:  22-MAY-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lehnhardt, Susan K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  31608-20001.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  15:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  918 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-862-124-15

  Query Match             78.8%;  Score 300.4;  DB 3;  Length 918;
  Best Local Similarity   88.9%;  Pred. No. 1.1e-85;
  Matches  338;  Conservative    0;  Mismatches   36;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||| |||||||||||||||||||||||||||||||||
Db        440 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 381

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||| ||||||| |||| ||  ||||||||||||||||||||||||
Db        380 CCTGTGCAGCCTCTGGATTCCCCTTCAGAAGCTTTGCTATGCACTGGGTCCGCCAGGCTC 321

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||| | ||||||||| |
Db        320 TAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCACTAAATACTACG 261

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||| |||||||||||| ||||||
Db        260 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGGTGTATC 201

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              | |||||||||||||||| |||||||||||||||| |||||||||||||| |||| |
Db        200 TAAAAATGAACAGCCTGAGAACTGAGGACACGGCTGTCTATTACTGTGCGAGAGATCAGA 141

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              |  |   ||| ||         || |||||||||||| |||||||||||||| ||||||
Db        140 GCCTGTTGGGTGACT------ATGACCACTACTACGGTTTGGACGTCTGGGGCAAAGGGA 87

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db         86 CCACGGTCACCGTCTCCTCA 67


RESULT 12
US-09-560-198A-1
; Sequence 1, Application US/09560198A
; Patent No. 6492497
; GENERAL INFORMATION:
;  APPLICANT: Thompson, Julia E
;  APPLICANT:  Lennard, Simon N
;  APPLICANT:  Wilton, Alison J
;  APPLICANT:  Braddock, Peta SH
;  APPLICANT:  Du Fou, Sarah L
;  APPLICANT:  McCafferty, John G
;  APPLICANT:  Conroy, Louise A
;  APPLICANT:  Tempest, Philip R
;  TITLE OF INVENTION: Specific binding members for TGFbeta1
;  FILE REFERENCE: 28111/35620A
;  CURRENT APPLICATION NUMBER: US/09/560,198A
;  CURRENT FILING DATE:  2000-04-28
;  PRIOR APPLICATION NUMBER: US 60/131,983
;  PRIOR FILING DATE: 1999-04-30
;  NUMBER OF SEQ ID NOS: 25
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 369
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-560-198A-1

  Query Match             78.6%;  Score 299.6;  DB 4;  Length 369;
  Best Local Similarity   89.2%;  Pred. No. 1.3e-85;
  Matches  339;  Conservative    0;  Mismatches   29;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| |  |||||||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTATTAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||||||||||||||||||||||||||||||  |  |
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGCGAACT---- 297

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                    |||  |  ||   |||| |       ||| ||||  ||||||| |||||||
Db        298 --------GGTGAATATAGTGGCTACGATACGAGTGGTGTGGAGCTCTGGGGGCAAGGGA 349

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        350 CCACGGTCACCGTCTCCTCA 369


RESULT 13
US-09-240-274-87
; Sequence 87, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
```

```
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 87
;   LENGTH: 381
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain D13
US-09-240-274-87

  Query Match             78.6%;  Score 299.4;  DB 3;  Length 381;
  Best Local Similarity   86.6%;  Pred. No. 1.5e-85;
  Matches  330;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
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Db         61 TCCTGTGCAGCGTCTGGATTCACCTTCAGTACTTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTTTGATGGAAGTAACAGAGACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
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Db        181 GCAGAGTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAAGTCCAAGAACACACTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
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Db        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACTCGGCTGTGTATTATTGTGCGAGAGAAAAT 300

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Db        301 GTGGCTCGTGGGGGGGGGGGCGTTCGATACAAGTACTACTTTGACTACTGGGGCCAGGGA 360

Qy        361 ACCACGGTCACCGTCTCCTCA 381.
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Db        361 ACCCTGGTCACCGTCTCCTCA 381


RESULT 14
US-08-862-124-18/c
; Sequence 18, Application US/08862124
; Patent No. 6207153
;  GENERAL INFORMATION:
;    APPLICANT:  Dan, Michael D.
;    APPLICANT:  Maiti, Pradip K.
;    APPLICANT:  Kaplan, Howard A.
;    TITLE OF INVENTION:  ANTIGEN BINDING FRAGMENTS H11, THAT
;    TITLE OF INVENTION:  SPECIFICALLY DETECT CANCER CELLS, NUCLEOTIDES ENCODING THE
;    TITLE OF INVENTION:  FRAGMENTS, AND USE THEREOF FOR THE PROPHYLAXIS AND
;    TITLE OF INVENTION:  DETECTION OF CANCERS
;    NUMBER OF SEQUENCES:  28
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Morrison & Foerster LLP
;      STREET:  755 Page Mill Road
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304-1018
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/862,124
;      FILING DATE:  22-MAY-1997
;      CLASSIFICATION:  424
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Lehnhardt, Susan K.
;      REGISTRATION NUMBER:  33,943
;      REFERENCE/DOCKET NUMBER:  31608-20001.20
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (650) 813-5600
;      TELEFAX:  (650) 494-0792
;      TELEX:  706141
;  INFORMATION FOR SEQ ID NO:  18:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  867 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-862-124-18

  Query Match             78.4%;  Score 298.8;  DB 3;  Length 867;
  Best Local Similarity   88.7%;  Pred. No. 3.3e-85;
  Matches  337;  Conservative    0;  Mismatches   37;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db        440 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 381

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
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Db        380 CCTGTGCAGCCTCTGGATTCCCCTTCAGAAGCTTTGCTATGCACTGGGTCCGCCAGGCTC 321

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        320 TAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCACTAAATACTACG 261

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        260 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACACTTCCAAGAACACGGTGTATC 201

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
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Qy        362 CCACGGTCACCGTCTCCTCA 381
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RESULT 15
US-09-240-274-86
; Sequence 86, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 86
;   LENGTH: 378
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain D12
US-09-240-274-86

Query Match 78.2%; Score 297.8; DB 3; Length 378;
Best Local Similarity 88.2%; Pred. No. 4.8e-85;
Matches 336; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

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              |||||||||||||||||||| ||||||||| ||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
                |||||||||| |||||||||| |||||| ||||||||||||||||||||||||||||||
Db         61 GCCTGTGCAGCGTCTGGATTCAGCTTCAGGAGCTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAGGGGGCTGGAGTGGGTGGCATTTACATGGTTTGATGGAAGCAATAAATATTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
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Db        181 GTAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||| |||||||||||||||||  || |||||||||| |||||||||||| |||    |
Db        241 CTGGAAATGAACAGCCTGAGAGTCGATGACACGGCTGTATATTACTGTGCGAGAGA---G 297

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
              | ||    | || | |   |   ||||||||||  |||||||||||||||| ||||
Db        298 GCGTCTATGCTTCGCGGAATTAGCAGATACTACTACGCGATGGACGTCTGGGGCCCAGGG 357

Qy        361 ACCACGGTCACCGTCTCCTCA 381
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Db        358 ACCACGGTCACCGTCTCCTCA 378
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Job time : 79.6581 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 08:53:09 ; Search time 327.469 Seconds
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6393.344 Million cell updates/sec

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Perfect score: 381
Sequence: 1 gaggtgcagctgctcgagtc.....ccacggtcaccgtctcctca 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	381	100.0	414	15	US-10-325-694-143	Sequence 143, App
2	325.6	85.5	379	16	US-10-309-762-211	Sequence 211, App
3	324.4	85.1	1413	14	US-10-153-382-16	Sequence 16, Appl
4	324.4	85.1	1413	18	US-10-612-497-61	Sequence 61, Appl
5	324.4	85.1	1413	18	US-10-776-649-61	Sequence 61, Appl
6	324	85.0	382	15	US-10-041-860-75	Sequence 75, Appl
7	324	85.0	382	17	US-10-665-383-45	Sequence 45, Appl
8	322.4	84.6	379	15	US-10-041-860-67	Sequence 67, Appl
9	322.4	84.6	379	17	US-10-665-383-29	Sequence 29, Appl
10	322.4	84.6	382	16	US-10-309-762-207	Sequence 207, App
11	322	84.5	370	16	US-10-269-711-42	Sequence 42, Appl
12	322	84.5	370	17	US-10-684-109-34	Sequence 34, Appl
13	320.8	84.2	379	15	US-10-041-860-59	Sequence 59, Appl
14	320.8	84.2	379	17	US-10-665-383-13	Sequence 13, Appl
15	320.4	84.1	370	16	US-10-269-711-10	Sequence 10, Appl
16	320.4	84.1	370	16	US-10-269-711-22	Sequence 22, Appl
17	320.4	84.1	370	16	US-10-269-711-26	Sequence 26, Appl
18	320.4	84.1	370	16	US-10-269-711-30	Sequence 30, Appl
19	320.4	84.1	370	16	US-10-269-711-34	Sequence 34, Appl
20	320.4	84.1	370	17	US-10-684-109-10	Sequence 10, Appl
21	318.8	83.7	370	16	US-10-269-711-6	Sequence 6, Appli
22	318.8	83.7	370	16	US-10-269-711-14	Sequence 14, Appl
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24	318.8	83.7	370	17	US-10-684-109-14	Sequence 14, Appl
25	318.8	83.7	2011	17	US-10-684-109-80	Sequence 80, Appl
c 26	318.8	83.7	2011	17	US-10-684-109-81	Sequence 81, Appl
27	318	83.5	487	16	US-10-395-894-30	Sequence 30, Appl
28	318	83.5	487	17	US-10-695-667-30	Sequence 30, Appl
29	318	83.5	7576	16	US-10-395-894-6	Sequence 6, Appli
30	318	83.5	7576	17	US-10-695-667-6	Sequence 6, Appli
31	317.6	83.4	372	15	US-10-371-942-81	Sequence 81, Appl
32	316.8	83.1	373	15	US-10-292-088-49	Sequence 49, Appl
33	316.4	83.0	376	15	US-10-292-088-57	Sequence 57, Appl
34	316.4	83.0	376	15	US-10-292-088-73	Sequence 73, Appl
35	316.4	83.0	1413	15	US-10-292-088-61	Sequence 61, Appl
36	315.2	82.7	373	15	US-10-292-088-95	Sequence 95, Appl
37	315.2	82.7	1410	15	US-10-292-088-53	Sequence 53, Appl
38	314.8	82.6	1413	15	US-10-292-088-77	Sequence 77, Appl
39	313.8	82.4	378	10	US-09-848-798-95	Sequence 95, Appl
40	312.8	82.1	378	15	US-10-292-088-91	Sequence 91, Appl
41	310.6	81.5	378	10	US-09-848-798-94	Sequence 94, Appl
42	310.6	81.5	378	10	US-09-848-798-196	Sequence 196, App
43	310.4	81.5	7561	16	US-10-395-894-7	Sequence 7, Appli
44	310.4	81.5	7561	17	US-10-695-667-7	Sequence 7, Appli
45	309.6	81.3	378	15	US-10-292-088-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-10-325-694-143
; Sequence 143, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 143
; LENGTH: 414
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-143

Query Match 100.0%; Score 381; DB 15; Length 414;
Best Local Similarity 100.0%; Pred. No. 2.3e-113;
Matches 381; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
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Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
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Qy        361 ACCACGGTCACCGTCTCCTCA 381
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RESULT 2
US-10-309-762-211
; Sequence 211, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 211
;   LENGTH: 379
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-211

  Query Match             85.5%;  Score 325.6;  DB 16;  Length 379;
  Best Local Similarity   92.9%;  Pred. No. 2.3e-95;
  Matches  353;  Conservative    0;  Mismatches   24;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
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Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
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Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 3
US-10-153-382-16
; Sequence 16, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
;   LENGTH: 1413
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-16

  Query Match             85.1%;  Score 324.4;  DB 14;  Length 1413;
  Best Local Similarity   92.9%;  Pred. No. 8.4e-95;
  Matches  353;  Conservative    0;  Mismatches   21;  Indels    6;  Gaps    1;

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Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||| |||||||||||||||||||||||||||||| ||||  |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGA 358

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || | |  |     |       ||||||||||||||||||||||||||||||||||||||||
Db        359 GGGGAGCTACCCTTT------ACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 412

Qy        362 CCACGGTCACCGTCTCCTCA 381
                ||||||||||||||||||||
Db        413 CCACGGTCACCGTCTCCTCA 432


RESULT 4
US-10-612-497-61
; Sequence 61, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV1
;  CURRENT APPLICATION NUMBER: US/10/612,497
;  CURRENT FILING DATE:  2003-07-01
```

```
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
;   LENGTH: 1413
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-612-497-61

  Query Match             85.1%;  Score 324.4;  DB 18;  Length 1413;
  Best Local Similarity   92.9%;  Pred. No. 8.4e-95;
  Matches  353;  Conservative    0;  Mismatches   21;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| |||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||| ||||  |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGA 358

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || | |  |    |       ||||||||||||||||||||||||||||||||||||
Db        359 GGGGAGCTACCCTTT------ACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 412

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        413 CCACGGTCACCGTCTCCTCA 432


RESULT 5
US-10-776-649-61
; Sequence 61, Application US/10776649
; Publication No. US20040228861A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV2
;  CURRENT APPLICATION NUMBER: US/10/776,649
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: US 10/612497
;  PRIOR FILING DATE: 2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 61
;   LENGTH: 1413
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-776-649-61

  Query Match             85.1%;  Score 324.4;  DB 18;  Length 1413;
  Best Local Similarity   92.9%;  Pred. No. 8.4e-95;
  Matches  353;  Conservative    0;  Mismatches   21;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| |||||||||||||||||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||| ||||  |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCGA 358

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              || | |  |    |       ||||||||||||||||||||||||||||||||||||
Db        359 GGGGAGCTACCCTTT------ACTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 412

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        413 CCACGGTCACCGTCTCCTCA 432


RESULT 6
US-10-041-860-75
; Sequence 75, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 75
;   LENGTH: 382
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-041-860-75

  Query Match             85.0%;  Score 324;  DB 15;  Length 382;
  Best Local Similarity   90.8%;  Pred. No. 7.5e-95;
  Matches  345;  Conservative    0;  Mismatches   35;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||| ||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
```

```
Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||| ||||||  |||||||||| | ||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGTATGATGGAAATGATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGCTTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||||| ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATT 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                |  |  ||| |       | ||||||||||||||||||||||||||||||||||||
Db        302 ACTATGATAGTAGTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        362 CCACGGTCACCGTCTCCTCA 381
```

RESULT 7
US-10-665-383-45
; Sequence 45, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce
; APPLICANT: LaRochelle, William
; APPLICANT: Lichenstein, Henri
; TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
; TITLE OF INVENTION: USING ANTI-PDGF-DD ANTIBODIES
; FILE REFERENCE: ABGENIX.052A
; CURRENT APPLICATION NUMBER: US/10/665,383
; CURRENT FILING DATE: 2003-09-16
; PRIOR APPLICATION NUMBER: 60/411,137
; PRIOR FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 45
; LENGTH: 382
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-665-383-45

Query Match 85.0%; Score 324; DB 17; Length 382;
Best Local Similarity 90.8%; Pred. No. 7.5e-95;
Matches 345; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

```
Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||| |||||||||| ||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| ||||||  |||||||||| | ||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAATTATATGGTATGATGGAAATGATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGCTTCACCGTCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||||| ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGATATT 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                |  |  ||| |       | ||||||||||||||||||||||||||||||||||||
Db        302 ACTATGATAGTAGTGATTATCTCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        362 CCACGGTCACCGTCTCCTCA 381
```

RESULT 8
US-10-041-860-67
; Sequence 67, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
; APPLICANT: Corvalan, Jose R.F.
; APPLICANT: Jia, Xiao-Chi
; APPLICANT: Feng, Xiao
; APPLICANT: Yang, Xiao-Dong
; APPLICANT: Chen, Francine
; APPLICANT: Gazit, Gadi
; APPLICANT: Weber, Richard
; APPLICANT: Bezabeh, Binyam
; TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: ABGENIX.051A
; CURRENT APPLICATION NUMBER: US/10/041,860
; CURRENT FILING DATE: 2002-01-07
; NUMBER OF SEQ ID NOS: 377
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 379
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-041-860-67

Query Match 84.6%; Score 322.4; DB 15; Length 379;
Best Local Similarity 92.4%; Pred. No. 2.5e-94;
Matches 351; Conservative 0; Mismatches 26; Indels 3; Gaps 1;

```
Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||| ||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||| ||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCAGTTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||| |||||| ||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||| ||||||| ||||  ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |   ||  ||| |       ||||||| ||||||||||||||||||||||||||||||
Db        302 GATACAGCTATGGTT---ACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378
```

RESULT 9
US-10-665-383-29
; Sequence 29, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
; APPLICANT: Floege, Juergen
; APPLICANT: Gazit, Gadi
; APPLICANT: Keyt, Bruce

```
;  APPLICANT:  LaRochelle, William
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
;  TITLE OF INVENTION:  USING ANTI-PDGF-DD ANTIBODIES
;  FILE REFERENCE: ABGENIX.052A
;  CURRENT APPLICATION NUMBER: US/10/665,383
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: 60/411,137
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 29
;   LENGTH: 379
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-665-383-29

  Query Match             84.6%;  Score 322.4;  DB 17;  Length 379;
  Best Local Similarity   92.4%;  Pred. No. 2.5e-94;
  Matches  351;  Conservative    0;  Mismatches   26;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||  |||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCAGTTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGATATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||| |||||||||||||||||| ||||||| ||||  ||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTATTGTGCGAGAGATCAGG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |   ||  ||| |       ||||||| ||||||||||||||||||||||||||||||
Db        302 GATACAGCTATGGTT---ACGTCTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 10
US-10-309-762-207
; Sequence 207, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 207
;   LENGTH: 382
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-207

  Query Match             84.6%;  Score 322.4;  DB 16;  Length 382;
  Best Local Similarity   90.5%;  Pred. No. 2.5e-94;
  Matches  344;  Conservative    0;  Mismatches   36;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||| ||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||| |||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGCCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||  |||||||||||| ||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTACTAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||| |||||||||||||||||||||||||||| ||||   |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCGAG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |       |   | ||      | |    ||||||||||||||||||||||||||||||
Db        302 GATTACTATGGTTCGGGGAGTTATCCCCACACTACGGTATGGACGTCTGGGGCCAAGGGA 361

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        362 CCACGGTCACCGTCTCCTCA 381


RESULT 11
US-10-269-711-42
; Sequence 42, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  DeVries, Peter J.
;  APPLICANT:  Reilly, Edward B.
;  APPLICANT:  Ostrow, Dave
;  APPLICANT:  Weiler, James
;  APPLICANT:  Green, Larry
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 6989.US.O1
;  CURRENT APPLICATION NUMBER: US/10/269,711
;  CURRENT FILING DATE:  2002-10-14
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 42
;   LENGTH: 370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-269-711-42

  Query Match             84.5%;  Score 322;  DB 16;  Length 370;
  Best Local Similarity   92.9%;  Pred. No. 3.3e-94;
  Matches  353;  Conservative    0;  Mismatches   15;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
```

```
Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        242 TGCAAATGAACAGCCTGAGAGTTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---- 297

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                  ||  ||||   |  |||| ||||||||||||||||||||||||||||||||||||
Db        298 --------CACGGTGGGAGGTACGTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 349

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        350 CCACGGTCACCGTCTCCTCA 369


RESULT 12
US-10-684-109-34
; Sequence 34, Application US/10684109
; Publication No. US20040175379A1
; GENERAL INFORMATION:
;  APPLICANT: DeVries, Peter J.
;  APPLICANT:  Green, Larry L.
;  APPLICANT:  Ostrow, David H.
;  APPLICANT:  Reilly, Edward B.
;  APPLICANT:  Wieler, James
;  TITLE OF INVENTION: Erythropoietin Receptor Binding
;  TITLE OF INVENTION:  Antibodies
;  FILE REFERENCE: 6989.US.02
;  CURRENT APPLICATION NUMBER: US/10/684,109
;  CURRENT FILING DATE:  2003-10-10
;  PRIOR APPLICATION NUMBER: 10/269,711
;  PRIOR FILING DATE: 2002-10-14
;  NUMBER OF SEQ ID NOS: 115
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 34
;   LENGTH: 370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-684-109-34

  Query Match            84.5%;  Score 322;  DB 17;  Length 370;
  Best Local Similarity  92.9%;  Pred. No. 3.3e-94;
  Matches  353;  Conservative    0;  Mismatches   15;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        242 TGCAAATGAACAGCCTGAGAGTTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---- 297

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                  ||  ||||   |  |||| ||||||||||||||||||||||||||||||||||||
Db        298 --------CACGGTGGGAGGTACGTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 349

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        350 CCACGGTCACCGTCTCCTCA 369


RESULT 13
US-10-041-860-59
; Sequence 59, Application US/10041860
; Publication No. US20030157109A1
; GENERAL INFORMATION:
;  APPLICANT: Corvalan, Jose R.F.
;  APPLICANT:  Jia, Xiao-Chi
;  APPLICANT:  Feng, Xiao
;  APPLICANT:  Yang, Xiao-Dong
;  APPLICANT:  Chen, Francine
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Weber, Richard
;  APPLICANT:  Bezabeh, Binyam
;  TITLE OF INVENTION: ANTIBODIES DIRECTED TO PDGFD AND USES
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: ABGENIX.051A
;  CURRENT APPLICATION NUMBER: US/10/041,860
;  CURRENT FILING DATE:  2002-01-07
;  NUMBER OF SEQ ID NOS: 377
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 59
;   LENGTH: 379
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-041-860-59

  Query Match            84.2%;  Score 320.8;  DB 15;  Length 379;
  Best Local Similarity  92.1%;  Pred. No. 8.2e-94;
  Matches  350;  Conservative    0;  Mismatches   27;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | |||||| |||||||||| ||||||||||||||| ||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||||||||| ||||   |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAAG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |    |||       |  ||||||| ||||||||||||||||||||||||||||||
Db        302 GAT---ACAGATATGCTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 14
US-10-665-383-13
; Sequence 13, Application US/10665383
; Publication No. US20040141969A1
; GENERAL INFORMATION:
;  APPLICANT: Ploege, Juergen
;  APPLICANT:  Gazit, Gadi
;  APPLICANT:  Keyt, Bruce
;  APPLICANT:  LaRochelle, William
;  APPLICANT:  Lichenstein, Henri
;  TITLE OF INVENTION: METHOD FOR THE TREATMENT OF NEPHRITIS
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;  TITLE OF INVENTION:  USING ANTI-PDGF-DD ANTIBODIES
;  FILE REFERENCE: ABGENIX.052A
;  CURRENT APPLICATION NUMBER: US/10/665,383
;  CURRENT FILING DATE:  2003-09-16
;  PRIOR APPLICATION NUMBER: 60/411,137
;  PRIOR FILING DATE: 2002-09-16
;  NUMBER OF SEQ ID NOS: 97
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13
;   LENGTH: 379
;   TYPE: DNA
;   ORGANISM: homo sapiens
US-10-665-383-13

  Query Match             84.2%;  Score 320.8;  DB 17;  Length 379;
  Best Local Similarity   92.1%;  Pred. No. 8.2e-94;
  Matches  350;  Conservative    0;  Mismatches   27;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | ||||| ||||||||| ||||||||||||| ||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCGGGGGGAGGCGTGGTCCAGCCTGGGAAGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||| ||||    |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATCAAG 301

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | |    |||         |   ||||||| ||||||||||||||||||||||||||||
Db        302 GAT---ACAGATATGCTGGTTACTACTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 358

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        359 CCACGGTCACCGTCTCCTCA 378


RESULT 15
US-10-269-711-10
; Sequence 10, Application US/10269711
; Publication No. US20040071694A1
; GENERAL INFORMATION:
;  APPLICANT: Abbott Laboratories
;  APPLICANT:  DeVries, Peter J.
;  APPLICANT:  Reilly, Edward B.
;  APPLICANT:  Ostrow, Dave
;  APPLICANT:  Weiler, James
;  APPLICANT:  Green, Larry
;  TITLE OF INVENTION: ERYTHROPOIETIN RECEPTOR BINDING
;  TITLE OF INVENTION:  ANTIBODIES
;  FILE REFERENCE: 6989.US.01
;  CURRENT APPLICATION NUMBER: US/10/269,711
;  CURRENT FILING DATE:  2002-10-14
;  NUMBER OF SEQ ID NOS: 57
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 10
;   LENGTH: 370
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-269-711-10

  Query Match             84.1%;  Score 320.4;  DB 16;  Length 370;
  Best Local Similarity   92.6%;  Pred. No. 1.1e-93;
  Matches  352;  Conservative    0;  Mismatches   16;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| ||||||||||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||||||| ||||
Db        242 TGCAAATGAACAGCCTGAGAGTTGAGGACACGGCTGTGTATTACTGTGCGAGAGAT---- 297

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                        ||  ||||   |  |||| ||||||||||||||||||||||||||||
Db        298 --------CACGGTGGGAGGTACGTCTACGACTACGGTATGGACGTCTGGGGCCAAGGGA 349

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        350 CCACGGTCACCGTCTCCTCA 369


Search completed: December  7, 2004, 14:26:30
Job time : 328.469 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 ; Search time 2223.46 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-143_COPY_1_381
Perfect score: 381
Sequence: 1 gaggtgcagctgctcgagtc.....ccacggtcaccgtctcctca 381

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	319.2	83.8	516	2	AW401728	AW401728 UI-HF-BK0
2	308	80.8	750	2	BF976111	BF976111 602244955
3	305.4	80.2	802	4	BG756245	BG756245 602713557
4	302.4	79.4	536	2	AW402624	AW402624 UI-HF-BK0
5	299.8	78.7	511	2	AW402453	AW402453 UI-HF-BK0
6	298.4	78.3	958	4	BG757665	BG757665 602711255
7	297.8	78.2	740	4	BG757947	BG757947 602714983
8	297.8	78.2	741	4	BG754024	BG754024 602709552
9	297.6	78.1	1007	4	BM914489	BM914489 AGENCOURT
10	294	77.2	663	4	BG686759	BG686759 602650729
11	293	76.9	912	4	BG756211	BG756211 602713521
12	292.2	76.7	846	4	BG755572	BG755572 602716255
13	292	76.6	876	4	BG758406	BG758406 602712604
14	292	76.6	907	5	BQ898892	BQ898892 AGENCOURT
15	291.6	76.5	788	4	BG342203	BG342203 602462979
16	291.2	76.4	678	4	BG340648	BG340648 602462226
17	291.2	76.4	870	4	BG759649	BG759649 602713342
18	291.2	76.4	964	2	BF663281	BF663281 602144406
19	291.2	76.4	991	2	BF974524	BF974524 602243430
20	291.2	76.4	1010	2	BF663436	BF663436 602144593
21	290	76.1	930	4	BG755605	BG755605 602716292
22	289.4	76.0	899	5	BQ420418	BQ420418 AGENCOURT
23	289.4	76.0	1228	4	BM920476	BM920476 AGENCOURT
24	287.8	75.5	456	4	BG503730	BG503730 602549705
25	287.8	75.5	902	5	BX436850	BX436850 BX436850
26	287.8	75.5	991	6	CD515249	CD515249 AGENCOURT
27	287.2	75.4	413	5	BX344075	BX344075 BX344075
28	285.6	75.0	942	5	BQ711102	BQ711102 AGENCOURT
29	284.4	74.6	894	5	BQ708235	BQ708235 AGENCOURT
30	283.8	74.5	430	5	BX480277	BX480277 DKFZp686O
31	283.6	74.4	979	5	BQ708029	BQ708029 AGENCOURT
32	282.8	74.2	761	4	BG757080	BG757080 602715111
33	281.4	73.9	621	6	CD687626	CD687626 EST4147 h
34	279.2	73.3	648	6	CD691229	CD691229 EST7752 h
35	278	73.0	897	4	BG685787	BG685787 602637892
36	278	73.0	907	5	BQ708724	BQ708724 AGENCOURT
37	278	73.0	1001	4	BM914366	BM914366 AGENCOURT
38	277.2	72.8	606	6	CD685360	CD685360 EST1880 h
39	277	72.7	503	2	AW402572	AW402572 UI-HF-BK0
40	277	72.7	881	4	BG686259	BG686259 602638142
41	276.2	72.5	509	6	CD684864	CD684864 EST1384 h
42	275.8	72.4	923	5	BQ711542	BQ711542 AGENCOURT
43	275.6	72.3	918	5	BQ710537	BQ710537 AGENCOURT
44	275.6	72.3	962	5	BQ706534	BQ706534 AGENCOURT
45	274.8	72.1	413	5	BX399298	BX399298 BX399298

ALIGNMENTS

RESULT 1
AW401728
LOCUS AW401728 516 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BK0-aaf-f-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3053711 5', mRNA sequence.
ACCESSION AW401728
VERSION AW401728.1 GI:6920414
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 516)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .516
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3053711"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

Query Match 83.8%; Score 319.2; DB 2; Length 516;
Best Local Similarity 91.8%; Pred. No. 4.7e-83;

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  Matches  349;  Conservative    0;  Mismatches   28;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||||| ||||||||||||||||||||||||||||||
Db        132 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 191

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||
Db        192 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTC 251

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        252 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTACG 311

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 371

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||| |||||||||||||||||||||||||||||||      |
Db        372 TGCAAATGAACAGCCTGAGAACTGAGGACACGGCTGTGTATTACTGTGCGAAAGCCCCTG 431

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                |   |  |     ||| ||||||||||||||||||||||||||||||||||||||||
Db        432 ---GTCCTACGGTGACTTCACCTTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 488

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||  |||
Db        489 CCACGGTCACCGTCTTTTCA 508


RESULT 2
BF976111
LOCUS       BF976111                750 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602244955F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4336308 5',
            mRNA sequence.
ACCESSION   BF976111
VERSION     BF976111.1  GI:12343326
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1208  row: m  column: 13
            High quality sequence stop: 732.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4336308"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             80.8%;  Score 308;  DB 2;  Length 750;
  Best Local Similarity   90.0%;  Pred. No. 1e-79;
  Matches  342;  Conservative    0;  Mismatches   35;  Indels    3;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db        122 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 181

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
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Db        182 CCTGTGCAGCCTCTGGATTCTCCTTTGGAAACTATGGCATGCACTGGGTCCGCCAGGCTC 241

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||| |||||||||||||||||| | ||||||||||||
Db        242 CAGGCAAGGGGCTGGAGTGGGTGGCTGTTATATCATATGATGGAATTTATAAATACTATG 301

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||  ||||
Db        302 GAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAAAACGGCGTATT 361

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||| |||||||||||||||| ||||||||||||||||||||||||||||||||    ||
Db        362 TGCAGATGAACAGCCTGAGAGGTGAGGACACGGCTGTGTATTACTGTGCGAAAGACTCGG 421

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
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Db        422 ---CCGACTGGAACTCCCATTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 478

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        479 CCACGGTCACCGTCTCCTCA 498


RESULT 3
BG756245
LOCUS       BG756245                802 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602713557F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853655 5',
            mRNA sequence.
ACCESSION   BG756245
VERSION     BG756245.1  GI:14066898
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 802)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1700  row: a  column: 16
            High quality sequence stop: 795.
FEATURES             Location/Qualifiers
     source          1. .802
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4853655"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
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                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             80.2%;  Score 305.4;  DB 4;  Length 802;
  Best Local Similarity   91.3%;  Pred. No. 6.1e-79;
  Matches  348;  Conservative    0;  Mismatches   26;  Indels    7;  Gaps    2;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db        129 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 188

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 248

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAA-GTAATAAATACTAT 180
              |||||||||||||||||||||||||| |||||   |||||||||| ||||||||||||||
Db        249 CAGGCAAGGGGCTGGAGTGGGTGGCATTTATACGGTATGATGGAACGTAATAAATACTAT 308

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 368

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
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Db        369 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAAGGA 428

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
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Db        429 GTGGGAGCTCCCCTGCGG------TACTACTACTATGGTATGGACGTCTGGGGCCAAGGG 482

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        483 ACCACGGTCACCGTCTCCTCA 503


RESULT 4
AW402624
LOCUS       AW402624                 536 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aax-h-08-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3055359 5', mRNA sequence.
ACCESSION   AW402624
VERSION     AW402624.1  GI:6921329
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 536)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Seq primer: M13 Forward.
FEATURES             Location/Qualifiers
     source          1. .536
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3055359"
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                     /cell_type="germinal center B cells"
                     /cell_line="MGC85"
                     /lab_host="DH10B (LTI)"
                     /clone_lib="NIH_MGC_36"
                     /note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
                     Constructed from size fractionated cytoplasmic mRNA
                     (0.5-1.5kb). Directionally cloned. Cells provided by Louis
                     M. Staudt, Ph.D. Library preparation by Maria de Fatima
                     Bonaldo, Ph.D.  and M. Bento Soares, Ph.D."
ORIGIN

  Query Match             79.4%;  Score 302.4;  DB 2;  Length 536;
  Best Local Similarity   89.5%;  Pred. No. 4.3e-78;
  Matches  340;  Conservative    0;  Mismatches   31;  Indels    9;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              | |||||||| | ||||||||||||||| ||||||| ||||||||||||||||||||||
Db         96 AAGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCATCCTGGGAGGTCCCTGAGACTCT 155

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||| |||||  ||||||||||||||||||||||
Db        156 CCTGTGCAGCCTCTGGATTCACCTTCAGTACCTATGCTATGCACTGGGTCCGCCAGGCTC 215

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| |
Db        216 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAGTAAATACTACG 275

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||  |||||
Db        276 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGGGGTATC 335

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||| |||||||||||||||||||| |||||||| ||||   |
Db        336 TGCAAATGAACAGCCTGAGAACTGAGGACACGGCTGTGTATTTCTGTGCGAGAGATTATG 395

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              | ||  |||           |||||||||||||  |||||| |||||||| ||||
Db        396 ACTCTGGTTTTGG---------GGACTACTACTACGGTTGGGACGTTTGGGGCCAGGGGA 446

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        447 CCACGGTCACCGTCTCCTCA 466


RESULT 5
AW402453
LOCUS       AW402453                 511 bp    mRNA    linear   EST 16-FEB-2000
DEFINITION  UI-HF-BK0-aan-f-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone
            IMAGE:3054479 5', mRNA sequence.
ACCESSION   AW402453
VERSION     AW402453.1  GI:6921139
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 511)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Eco RI site shown at the beginning of the sequence.
             Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: M.B. Soares Lab
             cDNA Library Arrayed by: M.B. Soares Lab
             DNA Sequencing by: M.B. Soares Lab
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES Location/Qualifiers
source 1. .511
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3054479"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 78.7%; Score 299.8; DB 2; Length 511;
Best Local Similarity 88.3%; Pred. No. 2.5e-77;
Matches 338; Conservative 0; Mismatches 42; Indels 3; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||| |||||||||| ||| ||||||||||||||||
Db         96 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCGGGGGGGTCCCTGAGACTCT 155

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||| || ||| |||||||| ||||||||||||||||||||||||||||||
Db        156 CCTGTGCAGCGTCTAGACTCAGCTTCAGTACCTATGGCATGCACTGGGTCCGCCAGGCTC 215

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||| |||||||||| |||||    |||||||||||||| |||||||||
Db        216 CAGGCAAGGGGCTGGGGTGGGTGGCACTTATACGGAATGATGGAAGTAATGAATACTATG 275

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 335

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA---GATA 298
              |||||||||||||||||||||||||||||||||||||||||| |||||||||   |
Db        336 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTATTGTGCGAAAGGCGCCC 395

Qy        299 TGGGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAG 358
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Db        396 GGGGACCGTGGAGTAGCAGCTCGATTCCCTACTACTACTACATGGACGTCTGGGGCAAAG 455

Qy        359 GGACCACGGTCACCGTCTCCTCA 381
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Db        456 GGACCACGGTCACCGTCTCCTCA 478
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RESULT 6
BG757665
LOCUS BG757665 958 bp mRNA linear EST 15-MAY-2001
DEFINITION 602711255F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4851661 5', mRNA sequence.
ACCESSION BG757665
VERSION BG757665.1 GI:14068318
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 958)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1694 row: n column: 14
High quality sequence stop: 799.

FEATURES Location/Qualifiers
source 1. .958
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4851661"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 78.3%; Score 298.4; DB 4; Length 958;
Best Local Similarity 88.4%; Pred. No. 7.4e-77;
Matches 336; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||| |||||||||| ||| ||||||||||||||||
Db        122 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 181

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||| |||||||  |||||| ||||||||||||||||||||||
Db        182 CCTGTGCAGCGTCTGGATTCAGCTTCAGTACGTATGGCTTGCACTGGGTCCGCCAGGCTC 241

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        242 CAGGCAAGGGGCTGGAGTGGGTGTCATTTATACGCTATGATGGAAGTAATAAATACTATG 301

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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              ||||||||| |||||||||||||| |||||||||||||||||||||||  |||||||
Db        362 TGCAAATGAGCAGCCTGAGAGCTGGGGACACGGCTGTGTATTACTGTGTAAAAGATA--- 418

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
              ||  ||   |||  |    | | |||||| ||| | ||||||||||||||||||||||
Db        419 GGGTGGATCGTGATAGTGACTACGATTACTACAACGCTTTGGACGTCTGGGGCCAAGGGA 478

Qy        362 CCACGGTCACCGTCTCCTCA 381
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Db        479 CCACGGTCACCGTCTCCTCA 498
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RESULT 7
BG757947
LOCUS BG757947 740 bp mRNA linear EST 15-MAY-2001
DEFINITION 602714983F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4854932 5', mRNA sequence.
ACCESSION BG757947
VERSION BG757947.1 GI:14068600
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 740)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1703  row: f  column: 21
            High quality sequence stop: 736.
FEATURES             Location/Qualifiers
     source          1. .740
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4854932"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             78.2%;  Score 297.8;  DB 4;  Length 740;
  Best Local Similarity   86.4%;  Pred. No. 1.1e-76;
  Matches  329;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
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Db         81 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 140

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||| |||||||||||||||||  ||   ||      |  | | ||||  | ||||||
Db        201 CCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTAGTACCATATACTAC 260

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
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Db        261 GCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTAT 320

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||  |||||||||||||||||||||||||||||| ||||
Db        321 CTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCC 380

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
                 |  ||| |    ||   |||||||||||||||||||||||||||||||||||||||
Db        381 ATATATTGTAGTAGTACCAGCTGCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 440

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
Db        441 ACCACGGTCACCGTCTCCTCA 461


RESULT 8
BG754024
LOCUS       BG754024                741 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602709552F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4846117 5',
            mRNA sequence.
ACCESSION   BG754024
VERSION     BG754024.1  GI:14064677
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 741)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1686  row: g  column: 14
            High quality sequence stop: 735.
FEATURES             Location/Qualifiers
     source          1. .741
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4846117"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             78.2%;  Score 297.8;  DB 4;  Length 741;
  Best Local Similarity   86.4%;  Pred. No. 1.1e-76;
  Matches  329;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60
              |||||||||||| | ||||||||||||||| |||| ||||||||| ||||||||||||||
Db         81 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 140

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||||
Db        141 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATAGCATGAACTGGGTCCGCCAGGCT 200

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||| |||||||||||||||||  ||   ||      |  | | ||||  | ||||||
Db        201 CCAGGGAAGGGGCTGGAGTGGGTTTCATACATTAGTAGTAGTAGTAGTACCATATACTAC 260

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              |||||||| ||||||||||||||||||||||||||||||||||| |||||||| | ||||||
Db        261 GCAGACTCTGTGAAGGGCCGATTCACCATCTCCAGAGACAATGCCAAGAACTCACTGTAT 320

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATG 300
              ||||||||||||||||||||||  |||||||||||||||||||||||||||||| ||||
Db        321 CTGCAAATGAACAGCCTGAGAGACGAGGACACGGCTGTGTATTACTGTGCGAGAGATCCC 380

Qy        301 GGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 360
                 |  ||| |    ||   |||||||||||||||||||||||||||||||||||||||
Db        381 ATATATTGTAGTAGTACCAGCTGCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGG 440

Qy        361 ACCACGGTCACCGTCTCCTCA 381
              ||||||||||||||||||||
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Db        441 ACCACGGTCACCGTCTCCTCA 461


RESULT 9
BM914489
LOCUS       BM914489               1007 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6615377 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480167
            5', mRNA sequence.
ACCESSION   BM914489
VERSION     BM914489.1  GI:19364868
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1007)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2002  row: j  column: 08
            High quality sequence stop: 638.
FEATURES             Location/Qualifiers
     source          1. .1007
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5480167"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             78.1%;  Score 297.6;  DB 4;  Length 1007;
  Best Local Similarity   86.9%;  Pred. No. 1.3e-76;
  Matches  346;  Conservative    0;  Mismatches   34;  Indels   18;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||| | |||||||||||| ||||||||||||||||
Db        125 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTAGTCCAGCCTGGGGGGTCCCTGAGACTCT 184

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||  |||||||||| ||||||||||||||||||||||||||
Db        185 CCTGTGCAGCGTCTGGATTCAGTTTCAGTAGCTACGGCATGCACTGGGTCCGCCAGGCTC 244

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||   ||||||||||||||||||||||||||
Db        245 CAGGCAAGGGGCTGGAGTGGGTGGCATTTATACGGTATGATGGAAGTAATAAATACTATG 304

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db        305 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCAGTATC 364

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        365 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATTTCT 424

Qy        302 GGTGGGGCAGTGGCTGGAGACC----------------CTACTACTACTACGGTATGG 343
              || |   ||||  |  |  |                  ||||||||| ||||   ||||
Db        425 ATTGTGTTGGTGGTAGCTGCTCCTCGTGGACTCGCCATTTCTACTACTTCTACTACATGG 484

Qy        344 ACGTCTGGGGCCAAGGGACCACGGTCACCGTCTCCTCA 381
              |||||||||| ||||||||||||||||||||||||||||
Db        485 ACGTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCA 522


RESULT 10
BG686759
LOCUS       BG686759               663 bp    mRNA    linear   EST 01-MAY-2001
DEFINITION  602650729F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4763215 5',
            mRNA sequence.
ACCESSION   BG686759
VERSION     BG686759.1  GI:13918156
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 663)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1618  row: i  column: 08
            High quality sequence stop: 659.
FEATURES             Location/Qualifiers
     source          1. .663
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4763215"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             77.2%;  Score 294;  DB 4;  Length 663;
  Best Local Similarity   87.9%;  Pred. No. 1.4e-75;
  Matches  334;  Conservative    0;  Mismatches   40;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||| ||||||||||||||||||||||||||||||
Db        129 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 188

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||||||||||||||||  ||||||||||||||||||||
Db        189 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTC 248

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAATAAATACTACG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        249 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAATAAATACTACG 308

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        309 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 368

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db        369 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATCTTT 428

Qy        302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
                | |   ||  |  |  | || |       |  |||       |  ||||||||| || |
Db        429 TTTCGTATAGCAGTGGCTGGCCATCGGGTACCCTCGG------CTACTGGGGCCAGGGAA 482

Qy        362 CCACGGTCACCGTCTCCTCA 381
              ||  ||||||||||||||||
Db        483 CCCTGGTCACCGTCTCCTCA 502


RESULT 11
BG756211
LOCUS       BG756211                912 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602713521F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853837 5',
            mRNA sequence.
ACCESSION   BG756211
VERSION     BG756211.1  GI:14066864
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1700  row: i  column: 06
            High quality sequence stop: 889.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4853837"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             76.9%;  Score 293;  DB 4;  Length 912;
  Best Local Similarity   95.3%;  Pred. No. 2.9e-75;
  Matches  302;  Conservative    0;  Mismatches   15;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||||| |||||||||||||||||||||||||||||
Db        121 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 180

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||||||||| ||||||||| ||||||||||||||||||
Db        181 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATGGCATGAACTGGGTCCGCCAGGCTC 240

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        241 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAATAATAAATACTATG 300

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 360

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |||| |
Db        361 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATTCGA 420

Qy        302 GGTGGGGCAGTGGCTGG 318
              |  ||||||||||
Db        421 TGCATAACAGTGGCTGG 437


RESULT 12
BG755572
LOCUS       BG755572                846 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602716255F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856628 5',
            mRNA sequence.
ACCESSION   BG755572
VERSION     BG755572.1  GI:14066225
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 846)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1707  row: m  column: 13
            High quality sequence stop: 752.
FEATURES             Location/Qualifiers
     source          1. .846
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4856628"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             76.7%;  Score 292.2;  DB 4;  Length 846;
  Best Local Similarity   95.8%;  Pred. No. 4.9e-75;
  Matches  300;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||||| |||||||||||||||||||||||||||||
Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189
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Qy          62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         190 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 249

Qy         122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         250 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 309

Qy         182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy         242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGACAAGATTGG 429

Qy         302 GGTGGGGCAGTGG 314
               || || ||| |
Db         430 TCTGAGGGAGTTG 442


RESULT 13
BG758406
LOCUS       BG758406                 876 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602712604F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853016 5',
            mRNA sequence.
ACCESSION   BG758406
VERSION     BG758406.1  GI:14069059
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 876)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1698  row: g  column: 01
            High quality sequence stop: 856.
FEATURES             Location/Qualifiers
     source          1. .876
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4853016"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           76.6%;  Score 292;  DB 4;  Length 876;
  Best Local Similarity   85.5%;  Pred. No. 5.7e-75;
  Matches  325;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy           2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
               ||||||| || | |||||||||||||| |||||||||||||| ||||||| |||||||
Db         122 AGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTAAGACTCT 181

Qy          62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
               |||||||||| |||||  |||||||| |||||| ||||||||||||||||||||||||||||
Db         182 CCTGTGCAGCGTCTGGGCTCACCTTCGGTAGCTTTGGCATGCACTGGGTCCGCCAGGCTC 241

Qy         122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
               |||||||||||||||||||||||||  | ||   | ||||||||||||||  || |||||
Db         242 CAGGCAAGGGGCTGGAGTGGGTGGCCTTAATTCGACATGATGGAAGTAACGAAGACTATA 301

Qy         182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         302 GAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 361

Qy         242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
               |||||||||||| |||||||||||||| |||||||||||| ||||||||||||
Db         362 TGCAAATGAACAACCTGAGAGCTGAGGACTCGGCTGTGTATCACTGTGCGAAAGACCGTA 421

Qy         302 GGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCCAAGGGA 361
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Db         422 CGATTTTTGGAGTGGTCCGTGACAGTTTTGACTACGGTATGGACGTCTGGGGCCAAGGGA 481

Qy         362 CCACGGTCACCGTCTCCTCA 381
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Db         482 CCACGGTCACCGTCTCCTCA 501


RESULT 14
BQ898892
LOCUS       BQ898892                 907 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8616374 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6302153
            5', mRNA sequence.
ACCESSION   BQ898892
VERSION     BQ898892.1  GI:22290906
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 907)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2519  row: c  column: 18
            High quality sequence stop: 651.
FEATURES             Location/Qualifiers
     source          1. .907
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6302153"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed  by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of  California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN
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  Query Match             76.6%;  Score 292;  DB 5;  Length 907;
  Best Local Similarity   86.8%;  Pred. No. 5.7e-75;
  Matches  335;  Conservative    0;  Mismatches   45;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
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Db        125 AGGTACAACTCGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGACGTCCCTGAGACTCT 184

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
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Db        185 CCTGTACAGCGTCTGGATTCACCTTCAGTCGCAATGGCATGCACTGGGTCCGCCAGGCTC 244

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        245 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTGAAAAATACTATG 304

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||| ||||||| ||| ||
Db        305 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAGGAACACGGTGTTTC 364

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGAT---- 297
              |||||||||| ||||||||||  || |||||||||||||||||||||||| ||||
Db        365 TGCAAATGAAGAGCCTGAGAGGCGATGACACGGCTGTGTATTACTGTGCGAGAGATCGGG 424

Qy        298 --ATGGGGTGGGGCAGTGGCTGGAGACCCTACTACTACTACGGTATGGACGTCTGGGGCC 355
                || ||||  |  | |  |    |   |||||| ||||   ||||||||||||||
Db        425 AAATCGGGTTTGATATTAATGGTGTCCGTCACTACTTCTACTACATGGACGTCTGGGGCA 484

Qy        356 AAGGGACCACGGTCACCGTCTCCTCA 381
              |||||||||||||||||||||||||
Db        485 AAGGGACCACGGTCACCGTCTCCTCA 510


RESULT 15
BG342203
LOCUS       BG342203                 788 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602462979F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575931 5',
            mRNA sequence.
ACCESSION   BG342203
VERSION     BG342203.1  GI:13148641
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1287  row: m  column: 20
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4575931"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             76.5%;  Score 291.6;  DB 4;  Length 788;
  Best Local Similarity   95.5%;  Pred. No. 7.3e-75;
  Matches  300;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGGCCTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||| ||||||||||||||||||||||||||||
Db        129 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 188

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 248

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 308

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 368

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATATGG 301
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db        369 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATTGGT 428

Qy        302 GGTGGGGCAGTGGC 315
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Db        429 CTGAGGGAGTTGAC 442


Search completed: December  7, 2004, 11:13:49
Job time : 2227.46 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 02:37:53 ; Search time 2104.27 Seconds
(without alignments)
8360.047 Million cell updates/sec

Title: US-09-403-107-145
Perfect score: 372
Sequence: 1 gaggtgcagctgctcgagtc.....ctccggatgtgttccctcta 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	372	100.0	372	6	A84378	A84378 Sequence 14
2	372	100.0	372	6	BD075295	BD075295 Novel met
3	305.4	82.1	362	9	HSA308463	AJ308463 Homo sapi
4	304.4	81.8	339	9	AJ627239	AJ627239 Homo sapi
5	300.6	80.8	339	9	AF035024	AF035024 Homo sapi
6	296.2	79.6	376	9	AF115111	AF115111 Homo sapi
7	291.8	78.4	345	9	AB063888	AB063888 Homo sapi
8	291.6	78.4	342	9	HSIGHVCA	Z31686 H.sapiens (
9	291.6	78.4	437	9	HSE5435	Z14203 H.sapiens r
10	290.4	78.1	675	6	AR454090	AR454090 Sequence
11	290	78.0	425	9	AY392931	AY392931 Homo sapi
12	288.8	77.6	675	6	AR454086	AR454086 Sequence
13	288.8	77.6	675	6	AR454102	AR454102 Sequence
14	288.2	77.5	677	6	AR454084	AR454084 Sequence
15	287.4	77.3	1392	6	BD185287	BD185287 Uses of a
16	287.4	77.3	1392	6	BD273694	BD273694 Human mon
17	287.4	77.3	1392	6	BD273723	BD273723 Human mon
18	287.4	77.3	1392	6	AR454371	AR454371 Sequence
19	287.4	77.3	1392	6	AR454400	AR454400 Sequence
20	287.4	77.3	1392	6	AX616564	AX616564 Sequence
21	287.2	77.2	675	6	AR454107	AR454107 Sequence
22	286.6	77.0	342	9	HSA579107	AJ579107 Homo sapi
23	286.4	77.0	414	6	A84376	A84376 Sequence 14
24	286.4	77.0	414	6	BD075294	BD075294 Novel met
25	286.4	77.0	660	6	AX232570	AX232570 Sequence
26	286	76.9	1395	6	BD185285	BD185285 Uses of a
27	286	76.9	1395	6	BD273692	BD273692 Human mon
28	286	76.9	1395	6	BD273721	BD273721 Human mon
29	286	76.9	1395	6	AR454369	AR454369 Sequence
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31	286	76.9	1395	6	AX616560	AX616560 Sequence
32	285.8	76.8	403	12	AF453221	AF453221 Synthetic
33	285.8	76.8	1392	6	BD185281	BD185281 Uses of a
34	285.8	76.8	1392	6	BD185283	BD185283 Uses of a
35	285.8	76.8	1392	6	BD273691	BD273691 Human mon
36	285.8	76.8	1392	6	BD273717	BD273717 Human mon
37	285.8	76.8	1392	6	BD273719	BD273719 Human mon
38	285.8	76.8	1392	6	AR454368	AR454368 Sequence
39	285.8	76.8	1392	6	AR454394	AR454394 Sequence
40	285.8	76.8	1392	6	AR454396	AR454396 Sequence
41	285.8	76.8	1392	6	AX616553	AX616553 Sequence
42	285.8	76.8	1392	6	AX616556	AX616556 Sequence
43	285.6	76.8	398	9	HSE55310	Z14168 H.sapiens r
44	285.4	76.7	345	9	AB067097	AB067097 Homo sapi
45	285.2	76.7	336	9	HSA579114	AJ579114 Homo sapi

ALIGNMENTS

RESULT 1
A84378
LOCUS A84378 372 bp DNA linear PAT 21-JAN-2000
DEFINITION Sequence 145 from Patent WO9846645.
ACCESSION A84378
VERSION A84378.1 GI:6733301
KEYWORDS .
SOURCE unidentified
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 372)
AUTHORS Kufer,P. and Raum,T.
TITLE NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND USES THEREOF
JOURNAL Patent: WO 9846645-A 145 22-OCT-1998;
KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES Location/Qualifiers
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CDS <1. .>372
/note="unnamed protein product"
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/db_xref="GI:6733302"
/translation="EVQLLESGGVVVQPGGSLRLSCAASGFTFDDYAMHWVRQAPGKG
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ORIGIN

Query Match 100.0%; Score 372; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 6.2e-109;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
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Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300
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Qy        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360
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Db        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360

Qy        361 GTGTTCCCTCTA 372
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Db        361 GTGTTCCCTCTA 372
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RESULT 2
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LOCUS BD075295 372 bp DNA linear PAT 27-AUG-2002
DEFINITION Novel method for the production of anti-human antigen receptors and uses thereof.
ACCESSION BD075295
VERSION BD075295.1 GI:22620898
KEYWORDS JP 2001519824-A/24.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 372)
AUTHORS Kufer,P. and Raum,T.
TITLE Novel method for the production of anti-human antigen receptors and uses thereof
JOURNAL Patent: JP 2001519824-A 24 23-OCT-2001;
MICROMET AG
COMMENT OS Homo sapiens (human)
PN JP 2001519824-A/24
PD 23-OCT-2001
PF 14-APR-1998 JP 1998543494
PR 14-APR-1997 EP 97106109.8
PI PETER KUFER,TOBIAS RAUM
PC C07K16/00,C07K16/30,A61K39/395
CC Novel method for the production of anti-human antigen CC receptors and uses
CC thereof
FH Key Location/Qualifiers
FT CDS (1). .(372).
FEATURES Location/Qualifiers
source 1. .372
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 100.0%; Score 372; DB 6; Length 372;
Best Local Similarity 100.0%; Pred. No. 6.2e-109;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300
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Qy        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360
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Db        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360

Qy        361 GTGTTCCCTCTA 372
              ||||||||||||
Db        361 GTGTTCCCTCTA 372
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RESULT 3
HSA308463
LOCUS HSA308463 362 bp mRNA linear PRI 06-FEB-2002
DEFINITION Homo sapiens partial mRNA for immunoglobulin heavy chain variable region (IGHV3 gene), clone TEG4.
ACCESSION AJ308463
VERSION AJ308463.1 GI:12734095
KEYWORDS IGHV3 gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Jacobin,M.J., Laroche-Traineau,J., Little,M., Keller,A., Peter,K., Welschof,M., Nurden,A. and Clofent-Sanchez,G.
TITLE Human IgG monoclonal anti-alpha(IIb)beta(3)-binding fragments derived from immunized donors using phage display
JOURNAL J. Immunol. 168 (4), 2035-2045 (2002)
MEDLINE 21681719
PUBMED 11823541
REFERENCE 2 (bases 1 to 362)
AUTHORS Clofent-Sanchez,G.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2001) Clofent-Sanchez G., UMR5533, Cnrs, Hopital Cardiologique, Av de Magellan, 33604 Pessac, FRANCE
FEATURES Location/Qualifiers
source 1. .362
/organism="Homo sapiens"
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/cell_type="B lymphocyte"
/clone_lib="combinatorial scFv IgG TE-pSEX81 library"
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gene 1. .362
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CDS <1. .>362
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ORIGIN

Query Match 82.1%; Score 305.4; DB 9; Length 362;
Best Local Similarity 92.5%; Pred. No. 2.2e-87;
Matches 334; Conservative 0; Mismatches 21; Indels 6; Gaps 1;

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Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||| | |||||||||||| |||||| ||||||||| ||||||||||||||
Db          1 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              |||||||||||||||||||||||||    |   ||||| ||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAATAAATACTAC 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAG--- 297
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAAAGTCT 300

Qy        298 ---GAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCT 354
                 | ||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        301 TACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCATCCACCAAGGCC 360

Qy        355 C 355
              |
Db        361 C 361
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RESULT 4
AJ627239
LOCUS AJ627239 339 bp mRNA linear PRI 30-JUN-2004
DEFINITION Homo sapiens partial mRNA for IgD immunoglobulin heavy chain variable region (IGHV3-30 gene), clone T3.3.13.
ACCESSION AJ627239
VERSION AJ627239.1 GI:49523851
KEYWORDS IGHV3-30 gene; immunoglobulin heavy chain; variable region.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Dono,M.
TITLE Characterization of a novel CD5+ B cell population
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 339)
AUTHORS Dono,M.
TITLE Direct Submission
JOURNAL Submitted (10-FEB-2004) Dono M., Oncologia Medica C, Istituto Nazionale Ricerca sul Cancro, L.go R. Benzi 10, Italy, 16132, ITALY
FEATURES Location/Qualifiers
source 1. .339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chromosome="14"
/clone="T3.3.13"
/cell_type="B cell"
/tissue_type="tonsil"
/rearranged
/country="Italy"
gene 1. .339
/gene="IGHV3-30"
CDS <1. .>339
/gene="IGHV3-30"
/codon_start=1
/product="immunoglobulin heavy chain variable region"
/protein_id="CAF28442.1"
/db_xref="GI:49523852"
/translation="QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKG
LEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKHPET
WGQGTLVTVSS"
V_region <1. .>339
/gene="IGHV3-30"
/product="immunoglobulin heavy chain variable region"
ORIGIN

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  Best Local Similarity   93.8%;  Pred. No. 4.7e-87;
  Matches  317;  Conservative    0;  Mismatches   21;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |   |||| ||||||||||||||||||||||
Db         62 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              ||||||||||||||||||||||||||||||||||||||||||||||||||| |    |
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAACATCCTG 301

Qy        302 GCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 339
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Db        302 AGACCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 339
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RESULT 5
AF035024
LOCUS AF035024 339 bp mRNA linear PRI 24-SEP-1999
DEFINITION Homo sapiens clone MCE11H myosin-reactive immunoglobulin heavy chain variable region mRNA, partial cds.
ACCESSION AF035024
VERSION AF035024.1 GI:5921600
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 339)
AUTHORS Wu,X., Liu,B., Van der Merwe,P.L., Kalis,N.N., Berney,S.M. and Young,D.C.
TITLE Myosin-reactive autoantibodies in rheumatic carditis and normal fetus
JOURNAL Clin. Immunol. Immunopathol. 87 (2), 184-192 (1998)
MEDLINE 98277139
PUBMED 9614934
REFERENCE 2 (bases 1 to 339)
AUTHORS Young,D.C.
TITLE Direct Submission
JOURNAL Submitted (19-NOV-1997) Department of Pathology and Laboratory Medicine, University of Texas Health Science Center, 6431 Fannin, Houston, TX 77030, USA
FEATURES Location/Qualifiers
source 1. .339
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="MCE11H"
CDS <1. .>339
/note="autoantibody"
/codon_start=1
/product="myosin-reactive immunoglobulin heavy chain variable region"
/protein_id="AAD56260.1"
/db_xref="GI:5921601"

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                     /translation="EVQLVESGGGVVQPGGSLRLSCAASGFTFSSYGMHWVRQAPGKG
                     LEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKDLNY
                     WGQGTLVTVSS"
ORIGIN

  Query Match             80.8%;  Score 300.6;  DB 9;  Length 339;
  Best Local Similarity   92.9%;  Pred. No. 7.9e-86;
  Matches  315;  Conservative    0;  Mismatches   24;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||  | ||||||||||||| |||||| |||||||||||||||||||||||
Db          1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||| ||||||||||||||    |    |||| ||||||||||||||||||||||
Db         61 TCCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||||| |||||    |||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCATTTATACGGTATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATCTT 300

Qy        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 339
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Db        301 AACTACTGGGGCCAGGGAACGCTGGTCACCGTCTCCTCA 339


RESULT 6
AF115111
LOCUS       AF115111                376 bp    mRNA    linear   PRI 04-JAN-2000
DEFINITION  Homo sapiens clone dn5 immunoglobulin heavy chain variable region
            mRNA, partial cds.
ACCESSION   AF115111
VERSION     AF115111.1  GI:4836305
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 376)
  AUTHORS   Smithson,S.L., Srivastava,N., Hutchins,W.A. and Westerink,M.A.
  TITLE     Molecular analysis of the heavy chain of antibodies that recognize
            the capsular polysaccharide of Neisseria meningitidis in hu-PBMC
            reconstituted SCID mice and in the immunized human donor
  JOURNAL   Mol. Immunol. 36 (2), 113-124 (1999)
  MEDLINE   99305028
   PUBMED   10378683
REFERENCE   2  (bases 1 to 376)
  AUTHORS   Smithson,S.L., Srivastava,N., Hutchins,W.A. and Westerink,M.A.J.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-DEC-1998) Medicine, Medical College of Ohio, 3000
            Arlington Ave, Toledo, OH 43614, USA
FEATURES             Location/Qualifiers
     source          1. .376
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="dn5"
                     /cell_type="B cell"
     CDS             <1. .>376
                     /codon_start=1
                     /product="immunoglobulin heavy chain variable region"
                     /protein_id="AAD30397.1"
                     /db_xref="GI:4836306"
                     /translation="QVQLVESGGGVVQPGRSLRLSCAASGFTFSSYGMHWVRQAPGKG
                     LEWVAVISYDGSNKYYADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCANLFNN
                     RGGYWGQGTLVTVSSASTKAPSV"
     V_region        1. .294
                     /note="V3-23"
     J_segment       313. .376
                     /note="JH4b"
ORIGIN

  Query Match             79.6%;  Score 296.2;  DB 9;  Length 376;
  Best Local Similarity   90.5%;  Pred. No. 2.1e-84;
  Matches  332;  Conservative    0;  Mismatches   23;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              ||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||    |    |||| |||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCG---------- 291
              ||||||||||||||||||||||| |||||||||| || ||||||||||
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGAACCTGTTTA 301

Qy        292 --AAAAAGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                || | || |||||||||||||| |||||||||||||||||||||||||  ||||||
Db        302 ATAACAGGGGAGGCTACTGGGGCCAAGGAACCCTGGTCACCGTCTCCTCAGCTTCCACCA 361

Qy        350 AGGCTCC 356
              |||| ||
Db        362 AGGCCCC 368


RESULT 7
AB063888
LOCUS       AB063888                345 bp    mRNA    linear   PRI 02-JUL-2002
DEFINITION  Homo sapiens IGH mRNA for immunoglobulin heavy chain VHDJ region,
            partial cds, clone:H238.
ACCESSION   AB063888
VERSION     AB063888.1  GI:21668977
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Akahori,Y., Iba,Y., Morino,K., Shinohara,M., Hirono,Y., Kakita,M.,
            Suzuki,K., Torii,H., Ukai,Y., Honda,T., Katsumi,H., Okada,J.,
            Miura,K. and Kurosawa,Y.
  TITLE     Construction and characterization of antibody libraries: isolation
            of therapeutic human antibodies and application to functional
            genomics
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 345)
  AUTHORS   Kurosawa,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-JUN-2001) Yoshikazu Kurosawa, Institute for
            Comprehensive Medical Science, Fujita Health University;
            Kutsukake-cho, Toyoake 470-1192, Japan
            (E-mail:kurosawa@fujita-hu.ac.jp, Tel:81-562-93-9387)
COMMENT     Please visit our web site
            URL:http://www.fujita-hu.ac.jp/immunity/.
FEATURES             Location/Qualifiers
     source          1. .345
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                     /mol_type="mRNA"
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                     /gene="IGH"
     CDS             <1. .>345
                     /gene="IGH"
                     /codon_start=1
                     /product="immunoglobulin heavy chain VHDJ region"
                     /protein_id="BAC01516.1"
                     /db_xref="GI:21668978"
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                     DYWGQGTLVTVSS"
ORIGIN

  Query Match             78.4%;  Score 291.8;  DB 9;  Length 345;
  Best Local Similarity   93.3%;  Pred. No. 5.6e-83;
  Matches  318;  Conservative    0;  Mismatches   17;  Indels    6;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA------ 294
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGGGCGG 300

Qy        295 AAGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 335
              |  |  | ||||||||||||||||||||||||||||||||||
Db        301 ACTGGGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 341


RESULT 8
HSIGHVCA
LOCUS       HSIGHVCA                342 bp    DNA     linear   PRI 05-AUG-1999
DEFINITION  H.sapiens (VHIL) gene for immunoglobulin heavy chain variable
            region.
ACCESSION   Z31686
VERSION     Z31686.1  GI:509782
KEYWORDS    immunoglobulin heavy chain; immunoglobulin heavy chain variable
            region.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Figini,M., Marks,J.D., Winter,G. and Griffiths,A.D.
  TITLE     In vitro assembly of repertoires of antibody chains on the surface
            of phage by renaturation
  JOURNAL   J. Mol. Biol. 239 (1), 68-78 (1994)
  MEDLINE   94254092
   PUBMED   8196048
REFERENCE   2  (bases 1 to 342)
  AUTHORS   Griffiths,A.D.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-MAR-1994) A.D. Griffiths, MRC Centre for Protein
            Engineering, Hills Road, Cambridge, CB2 2QH, U.K
FEATURES             Location/Qualifiers
     source          1. .342
                     /organism="Homo sapiens"
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                     /dev_stage="adult"
     CDS             1. .342
                     /note="Protein sequence is in conflict with the conceptual
                     translation"
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                     /protein_id="CAA83491.1"
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                     /translation="EVQLVESGGGVVQPGRSLRLSCAASGFTFSSYAMHWVRQAPGKG
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                     YWGQGTLVTVSS"
ORIGIN

  Query Match             78.4%;  Score 291.6;  DB 9;  Length 342;
  Best Local Similarity   93.5%;  Pred. No. 6.5e-83;
  Matches  316;  Conservative    0;  Mismatches   19;  Indels    3;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
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Db          1 GAGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA---G 297
              |||||||||||||||||||||| |||||||||||||||||||||||||||||| | |   |
Db        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACTGG 300

Qy        298 GAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTC 335
              | || |||||||||||||||||||||||||||||| ||
Db        301 GGAGACTACTGGGGCCAGGGAACCCTGGTCACCGTGTC 338


RESULT 9
HSE5435
LOCUS       HSE5435                 437 bp    mRNA    linear   PRI 15-MAR-1993
DEFINITION  H.sapiens rearranged Ig heavy chain variable region (VDJ).
ACCESSION   Z14203 X65741
VERSION     Z14203.1  GI:30965
KEYWORDS    Ig D-segment; Ig heavy chain; Ig J-segment; Ig V-segment; Ig
            variable region; immunoglobulin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 437)
  AUTHORS   Cuisinier,A.M., Gauthier,L., Boubli,L., Fougereau,M. and
            Tonnelle,C.
  TITLE     Mechanisms that generate human immunoglobulin diversity operate
            from the 8th week of gestation in fetal liver
  JOURNAL   Eur. J. Immunol. 23 (1), 110-118 (1993)
  MEDLINE   93122076
   PUBMED   8419161
REFERENCE   2  (bases 1 to 437)
  AUTHORS   Tonnelle,C.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-JUN-1992) C. Tonnelle, Centre d'Immunologie
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          Marseille-Luminy, Case 906, 13288 Marseille Cedex 9, FRANCE
FEATURES             Location/Qualifiers
     source          1. .437
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                     /db_xref="taxon:9606"
                     /chromosome="14"
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                     /clone_lib="E54"
     CDS             36. .>437
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                     /db_xref="GI:30966"
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                     NSLRAEDTAVYYCARESRGDYWGQGTLVTVSS"
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                     /note="signal-peptide site"
     misc_feature    93. .386
                     /note="Ig V-segment"
     misc_feature    387. .398
                     /note="Ig D-segment"
     misc_feature    399. .437
                     /note="Ig J-segment"
ORIGIN

  Query Match             78.4%;  Score 291.6;  DB 9;  Length 437;
  Best Local Similarity   92.7%;  Pred. No. 6.8e-83;
  Matches  319;  Conservative    0;  Mismatches   19;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||||
Db         94 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 153

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |||||  |||||||||||||||||||||||
Db        154 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTC 213

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||| |
Db        214 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGCAATAAATACTACG 273

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 333

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAG---- 297
              |||||||||||||||||||||||||||||||||||||||||||||||||||| | ||
Db        334 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGAGAGCC 393

Qy        298 --GAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 339
                |  | ||||||||||||||||||||||||||||||||||||
Db        394 GAGGGGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 437


RESULT 10
AR454090
LOCUS       AR454090                675 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 67 from patent US 6680209.
ACCESSION   AR454090
VERSION     AR454090.1  GI:42686937
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 675)
  AUTHORS   Buechler,J., Valkirs,G., Gray,J. and Lonberg,N.
  TITLE     Human antibodies as diagnostic reagents
  JOURNAL   Patent: US 6680209-A 67 20-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .675
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             78.1%;  Score 290.4;  DB 6;  Length 675;
  Best Local Similarity   87.4%;  Pred. No. 1.8e-82;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||| |||||  |||||||||||||| | |||| |||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 11
AY392931
LOCUS       AY392931                425 bp    mRNA    linear   PRI 04-JUN-2004
DEFINITION  Homo sapiens clone RA702-A3-8.fa immunoglobulin heavy chain mRNA,
            partial cds.
ACCESSION   AY392931
VERSION     AY392931.1  GI:46253797
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 425)
  AUTHORS   Miura,Y., Chu,C.C., Dines,D.M., Asnis,S.E., Furie,R.A. and
            Chiorazzi,N.
  TITLE     Diversification of the Ig variable region gene repertoire of
            synovial B lymphocytes by nucleotide insertion and deletion
  JOURNAL   Mol. Med. 9 (5-8), 166-174 (2003)
  MEDLINE   22933091
   PUBMED   14571324
REFERENCE   2  (bases 1 to 425)
  AUTHORS   Miura,Y., Chu,C.C., Dines,D.M., Krauss,E.S., Asnis,S.E., Furie,R.A.
            and Chiorazzi,N.
  TITLE     Direct Submission
  JOURNAL   Submitted (17-SEP-2003) Center for Immunology and Inflammation,
            North Shore - LIJ Research Institute, 350 Community Drive,
            Manhasset, NY 11030, USA
FEATURES             Location/Qualifiers
     source          1. .425
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /isolate="RA702"
                     /db_xref="taxon:9606"
                     /clone="RA702-A3-8.fa"
                     /cell_type="B lymphocyte"
                     /tissue_type="rheumatoid arthritis synovial tissue"
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                     /note="IgA"
                     /codon_start=3
                     /product="immunoglobulin heavy chain"
                     /protein_id="AAS85871.1"
                     /db_xref="GI:46253798"
                     /translation="WVFLVALLRGVQCQVQLVESGGGVVQPGGSLRLSCAASGFTFSS
                     YGMHWVRQAPGKGLEWVAFIRYDGSNKYYADSVKGRFTISRDNSKNTLYLQMSSLRAE
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ORIGIN

  Query Match           78.0%;  Score 290;  DB 9;  Length 425;
  Best Local Similarity  87.8%;  Pred. No. 2.2e-82;
  Matches  330;  Conservative    0;  Mismatches   40;  Indels    6;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||  ||||||  |||||||||||||||||||||||
Db         43 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 102

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||||||||    |    ||||  ||||||||||||||||||||
Db        103 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 162

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||  |||||    |||||||||||||||||||||| |
Db        163 CAGGCAAGGGGCTGGAGTGGGTGGCATTTATACGGTATGATGGAAGTAATAAATACTACG 222

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        223 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 282

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA------A 295
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        283 TGCAAATGAGCAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGTCGGGT 342

Qy        296 AGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTC 355
                |    || |||||||||||||||||||||||||||||||| ||| || | |     |
Db        343 TTGGGAACTTCTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCGGCATCCCCGACCAGCC 402

Qy        356 CGGATGTGTTCCCTCT 371
              |  | ||  |||||  ||
Db        403 CCAAGGTCTTCCCGCT 418


RESULT 12
AR454086
LOCUS       AR454086                675 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 59 from patent US 6680209.
ACCESSION   AR454086
VERSION     AR454086.1  GI:42686933
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 675)
  AUTHORS   Buechler,J., Valkirs,G., Gray,J. and Lonberg,N.
  TITLE     Human antibodies as diagnostic reagents
  JOURNAL   Patent: US 6680209-A 59 20-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .675
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           77.6%;  Score 288.8;  DB 6;  Length 675;
  Best Local Similarity  87.2%;  Pred. No. 5.9e-82;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||  ||||||  |||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||||||||    |    ||||  ||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||  |||||    |||||||||||||||||||||| |
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | |||  ||||||||||||||||||||||||||||||||||||   ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||     || |||||  ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 13
AR454102
LOCUS       AR454102                675 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 91 from patent US 6680209.
ACCESSION   AR454102
VERSION     AR454102.1  GI:42686949
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 675)
  AUTHORS   Buechler,J., Valkirs,G., Gray,J. and Lonberg,N.
  TITLE     Human antibodies as diagnostic reagents
  JOURNAL   Patent: US 6680209-A 91 20-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .675
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match           77.6%;  Score 288.8;  DB 6;  Length 675;
  Best Local Similarity  87.2%;  Pred. No. 5.9e-82;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||  ||||||  |||||||||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||||||||    |    ||||  ||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||  |||||    |||||||||||||||||||||| |
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||||||  ||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
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Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
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              ||| ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 14
AR454084
LOCUS       AR454084                677 bp    DNA     linear   PAT 20-FEB-2004
DEFINITION  Sequence 55 from patent US 6680209.
ACCESSION   AR454084
VERSION     AR454084.1  GI:42686931
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 677)
  AUTHORS   Buechler,J., Valkirs,G., Gray,J. and Lonberg,N.
  TITLE     Human antibodies as diagnostic reagents
  JOURNAL   Patent: US 6680209-A 55 20-JAN-2004;
FEATURES             Location/Qualifiers
     source          1. .677
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ORIGIN

  Query Match             77.5%;  Score 288.2;  DB 6;  Length 677;
  Best Local Similarity   86.9%;  Pred. No. 9.2e-82;
  Matches  333;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
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Db          3 GATGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 62

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
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Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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Db        123 CCAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTAT 182

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 242

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG-- 298
              |||||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        243 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGG 302

Qy        299 ----------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACC 348
                       | ||| ||||||||||||||||||||||||||||||||  |||||
Db        303 ATCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 362

Qy        349 AAGGCTCCGGATGTGTTCCCTCT 371
              ||||  ||    || ||||| ||
Db        363 AAGGGCCCATCGGTCTTCCCCCT 385


RESULT 15
BD185287
LOCUS       BD185287                1392 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Uses of anti-CTLA-4 antibodies.
ACCESSION   BD185287
VERSION     BD185287.1  GI:31877487
KEYWORDS    JP 2002371013-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1392)
  AUTHORS   Douglas,C.H. and Mueller,E.E.
  TITLE     Uses of anti-CTLA-4 antibodies
  JOURNAL   Patent: JP 2002371013-A 7 26-DEC-2002;
            PFIZER PRODUCTS INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002371013-A/7
            PD   26-DEC-2002
            PF   17-MAY-2002 JP 2002142978
            PR   23-MAY-2001 US    60/293042
            PI   CHARLES HANSSON DOUGLAS,EILEEN ELLIOTT MUELLER PC
            A61K39/395,A61K38/00,A61P35/00//C07K16/18
            CC   Uses of anti-CTLA-4 antibodies
            FH   Key             Location/Qualifiers
            FT   source          1. .1392
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .1392
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ORIGIN

  Query Match             77.3%;  Score 287.4;  DB 6;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 1.9e-81;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||  ||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | ||||| ||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||| |   | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
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Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
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GenCore version 5.1.6

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Searched: 4134886 seqs, 2624710521 residues

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	288.8	77.6	675	4	AAH41673	Aah41673 Human int
7	288.8	77.6	675	4	AAH41657	Aah41657 Human int
8	288.8	77.6	675	4	AAH30003	Aah30003 Anti-IL8
9	288.8	77.6	675	4	AAH30019	Aah30019 Anti-IL8
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15	287.4	77.3	1392	10	AAD54347	Aad54347 Human 6.1
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19	286.4	77.0	414	2	AAV68537	Aav68537 Nucleotid
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21	286	76.9	1395	3	AAA46866	Aaa46866 DNA encod
22	286	76.9	1395	3	AAA46894	Aaa46894 DNA encod
23	286	76.9	1395	10	AAD54345	Aad54345 Human 4.8
24	285.8	76.8	1392	3	AAA46864	Aaa46864 DNA encod
25	285.8	76.8	1392	3	AAA46890	Aaa46890 cDNA enco
26	285.8	76.8	1392	3	AAA46892	Aaa46892 DNA encod
27	285.8	76.8	1392	10	AAD54341	Aad54341 Human 4.1
28	285.8	76.8	1392	10	AAD54343	Aad54343 Human 4.1
29	285.6	76.8	675	4	AAH30059	Aah30059 TRO005 he
30	285.6	76.8	675	4	AAH30062	Aah30062 TRO005 he
31	284.4	76.5	357	12	ADI26655	Adi26655 Human ant
32	284.2	76.4	1999	3	AAA46891	Aaa46891 DNA encod
33	284.2	76.4	1999	10	AAD54342	Aad54342 Human 4.1
34	284	76.3	351	12	ADI22042	Adi22042 Anti-plat
35	284	76.3	351	12	ADI22043	Adi22043 Anti-plat
36	284	76.3	675	4	AAH41681	Aah41681 Human int
37	284	76.3	675	4	AAH30027	Aah30027 Anti-IL8
38	283.8	76.3	405	10	ADC61031	Adc61031 Human ant
39	282.4	75.9	351	12	ADI22044	Adi22044 Anti-plat
40	282.4	75.9	351	12	ADI22041	Adi22041 Anti-plat
41	282.4	75.9	675	4	AAH41682	Aah41682 Human int
42	282.4	75.9	675	4	AAH41677	Aah41677 Human int
43	282.4	75.9	675	4	AAH41680	Aah41680 Human int
44	282.4	75.9	675	4	AAH30026	Aah30026 Anti-IL8
45	282.4	75.9	675	4	AAH30023	Aah30023 Anti-IL8

ALIGNMENTS

RESULT 1
AAV68538
ID AAV68538 standard; DNA; 372 BP.
XX
AC AAV68538;
XX
DT 16-FEB-1999 (first entry)
XX
DE Nucleotide sequence of human D7.2 heavy chain variable region.
XX
KW Human; D7.2 heavy chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .372
FT /*tag= a
FT /product= "human D7.2 heavy chain variable region"
XX
PN WO9846645-A2.
XX
PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-EP002180.
XX
PR 14-APR-1997; 97EP-00106109.
XX
PA (KUFE/) KUFER P.
PA (RAUM/) RAUM T.
XX
PI Kufer P, Raum T;
XX
DR WPI; 1998-594564/50.
DR P-PSDB; AAW80816.
XX
PT Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.
XX
PS Claim 9; Fig 8; 84pp; English.
XX
CC This is the nucleotide sequence of the human D7.2 heavy chain variable

```
CC   region, used in the method of the invention. for providing receptors that
CC   can be used for targeting antigens in humans without being immunogenic
CC   themselves. Such receptors can be used for treating diseases such as
CC   tumours or auto-immune diseases, graft rejection after transplantation,
CC   infectious diseases by targeting cellular receptors as well as allergic,
CC   inflammatory, endocrine and degenerative diseases by targeting key
CC   molecules involved in the pathological process
XX
SQ   Sequence 372 BP; 86 A; 95 C; 110 G; 81 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 372;  DB 2;  Length 372;
  Best Local Similarity   100.0%;  Pred. No. 3.7e-100;
  Matches  372;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300

Qy        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360

Qy        361 GTGTTCCCTCTA 372
              ||||||||||||
Db        361 GTGTTCCCTCTA 372


RESULT 2
ADN07003
ID   ADN07003 standard; DNA; 729 BP.
XX
AC   ADN07003;
XX
DT   01-JUL-2004  (first entry)
XX
DE   Human EFGR bs-scFv antibody associated DNA.
XX
KW   Bispecific single chain; bs-scFv; cancer;
KW   epidermal growth factor receptor; EGFR; therapy; antibody; human; ds.
XX
OS   Homo sapiens.
XX
PN   US2004071696-A1.
XX
PD   15-APR-2004.
XX
PF   04-APR-2003; 2003US-00406830.
XX
PR   05-APR-2002; 2002US-0370276P.
XX
PA   (REGC ) UNIV CALIFORNIA.
PA   (FOXC-) FOX CHASE CANCER CENT.
XX
PI   Adams GP,  Horak EM,  Weiner LM,  Marks JD;
XX
DR   WPI; 2004-328525/30.
XX
PT   Novel bispecific antibody comprising first and second antibody joined to
PT   each other and having binding specificity to different epitopes of
PT   Epidermal Growth Factor Receptor protein, useful for treating cancer.
XX
PS   Claim 14; SEQ ID NO 20; 57pp; English.
XX
CC   The present invention provides bispecific single chain (bs-scFv) antibody
CC   molecules which may be used to treat various forms of cancer associated
CC   with the overexpression of the epidermal growth factor receptor (EGFR)
CC   family. The invention is useful for specifically delivering an effector
CC   molecule to a cell bearing a receptor from EGFR protein family chosen
CC   from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
CC   treatment of cancer. The present sequence is human EFGR bs-scFv antibody
CC   associated DNA used in the invention.
XX
SQ   Sequence 729 BP; 155 A; 196 C; 216 G; 162 T; 0 U; 0 Other;

  Query Match             81.2%;  Score 302.2;  DB 12;  Length 729;
  Best Local Similarity   93.2%;  Pred. No. 2.4e-79;
  Matches  316;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          8 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 67

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||||
Db         68 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 127

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 187

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 247

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              |||||||||||||||||||||||||||||||||||| ||||||||||||||   |
Db        248 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGAGTATTACTGTGCGAAGTATCCTT 307

Qy        302 GCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 340
                |||||||||||||||||||||||||||||||||||
Db        308 TAAACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 346


RESULT 3
ADC61027
ID   ADC61027 standard; DNA; 396 BP.
XX
AC   ADC61027;
XX
DT   18-DEC-2003  (first entry)
XX
DE   Human anti-CD45RB monoclonal antibody DNA, SEQ ID No 54.
XX
KW   monoclonal antibody; CD45RB; antigen; cell proliferation;
KW   immunosuppressive; neuroprotective; tissue rejection; organ rejection;
KW   autoimmune disease; multiple sclerosis; human; anti-CD45RB; gene; ds.
XX
OS   Homo sapiens.
XX
PN   WO2003048327-A2.
XX
PD   12-JUN-2003.
XX
PF   02-DEC-2002; 2002WO-US038540.
XX
PR   03-DEC-2001; 2001US-0337276P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Foltz I,  Babcook J,  Palathumpat V,  Yang X,  King CT;
```

XX
DR WPI; 2003-558954/52.
DR P-PSDB; ADC61028.
XX
PT New anti-CD45RB monoclonal antibody, useful for treating an autoimmune
PT disease e.g. multiple sclerosis.
XX
PS Disclosure; SEQ ID NO 54; 121pp; English.
XX
CC The invention relates to a novel isolated monoclonal antibody comprising
CC a heavy chain having a sequence chosen from one of 22 fully defined
CC sequences comprising 135-147 amino acids, given in the specification, and
CC is specific for CD45RB antigen. The invention further relates to:
CC inhibiting cell proliferation associated with the expression of CD45RB
CC antigen; and treating a disease associated with the expression of a
CC CD45RB antigen in a patient. The monoclonal antibody has the activities
CC of immunosuppressive and neuroprotective. The monoclonal antibody is
CC useful for treating the rejection of a mammalian cell, tissue or organ,
CC especially an autoimmune disease in a mammal, especially a human e.g.
CC multiple sclerosis. This polynucleotide sequence represents a DNA
CC encoding a human protein of the anti-CD45RB monoclonal antibody of the
CC invention.
XX
SQ Sequence 396 BP; 84 A; 92 C; 124 G; 96 T; 0 U; 0 Other;

Query Match 79.2%; Score 294.8; DB 10; Length 396;
Best Local Similarity 92.0%; Pred. No. 3.1e-77;
Matches 311; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

```
Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||| ||||||  |||||||| ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||||  ||||||||||||| | || |||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCTGTTATATGGTATGATGGAAGTAAGAGATTCTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              |||||||||||||||||||| |||||||||||||||||||||||||| ||    ||
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAACTACAG 358

Qy        302 GCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 339
              |||||||||||||||||| ||||||||||||||||
Db        359 ACTACTGGGGCCAGGGAACCATGGTCACCGTCTCCTCA 396
```

RESULT 4
AAH41661
ID AAH41661 standard; DNA; 675 BP.
XX
AC AAH41661;
XX
DT 28-AUG-2001 (first entry)
XX
DE Human interleukin 8 antibody nucleotide sequence M1-23H.
XX
KW Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW target antigen; bacterial; fungal; viral; pathogen; human disease;
KW hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
XX
OS Homo sapiens.
OS Synthetic.
XX

PN WO200140306-A1.
XX
PD 07-JUN-2001.
XX
PF 06-DEC-2000; 2000WO-US033042.
XX
PR 06-DEC-1999; 99US-00456090.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR WPI; 2001-374798/39.
XX
PT Detecting analyte in human sample containing human antibodies binding to
PT nonhuman-antibodies, involves contacting sample with human antibody which
PT binds to antibodies from nonhuman species and detecting binding.
XX
PS Example 22; Page 88; 135pp; English.
XX
CC The present invention describes a method for detecting an analyte in a
CC human sample containing human antibodies that specifically bind to
CC antibodies from a nonhuman species. The method involves contacting the
CC sample with a human antibody (I) which specifically binds to antibodies
CC from a nonhuman species and detecting the binding between (I) and the
CC analyte to indicate presence of the analyte. The method is used for
CC detecting an analyte in a human sample containing human anti-mouse
CC antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC heterophilic antibodies). The method can also be used for detecting any
CC type of target antigen including bacterial, fungal and viral pathogens
CC that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC aeruginosa. Human antibodies can be used as detection reagents for
CC performing clinical diagnostic tests and for performing other in vitro
CC detection assays, including for research purposes. (I) can be used in
CC qualitative assays designed to indicate the presence of one or more
CC target antigens above minimally detectable amounts of antigen in the
CC sample that usually correspond to the sensitivity limitations of the
CC assays for each target antigen. Also, (I) is used to determine the amount
CC of target antigen in a sample in a semi-quantitative or relative sense.
CC Quantification of one or more target antigens in a sample can also be
CC carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 U; 0 Other;

Query Match 78.1%; Score 290.4; DB 4; Length 675;
Best Local Similarity 87.4%; Pred. No. 7.4e-76;
Matches 334; Conservative 0; Mismatches 36; Indels 12; Gaps 1;

```
Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  |  |||||||||||| |||||| ||||||||  ||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||||||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||| | |||| |||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||||||||||||||||||||||||||||||||||||||||  ||||||
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Db        302 TAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 5
AAH30007
ID   AAH30007 standard; DNA; 675 BP.
XX
AC   AAH30007;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody nucleotide fragment M1-23H.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027237.
XX
PR   02-OCT-1999;   99US-0157415P.
PR   01-DEC-1999;   99US-00453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS   Example 22; Page 92; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 675 BP; 151 A; 211 C; 188 G; 125 T; 0 U; 0 Other;

  Query Match             78.1%;  Score 290.4;  DB 4;  Length 675;
  Best Local Similarity   87.4%;  Pred. No. 7.4e-76;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  |  |||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||| |||||||||||||   | | |||| |||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||| |||||  |||||||||||||| | |||| |||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | |||||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 6
AAH41673
ID   AAH41673 standard; DNA; 675 BP.
XX
AC   AAH41673;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Human interleukin 8 antibody nucleotide sequence M2-11H.
XX
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033042.
XX
PR   06-DEC-1999;   99US-00456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding to
PT   nonhuman-antibodies, involves contacting sample with human antibody which
PT   binds to antibodies from nonhuman species and detecting binding.
XX
PS   Example 22; Page 90-91; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
```

```
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the amount
CC   of target antigen in a sample in a semi-quantitative or relative sense.
CC   Quantification of one or more target antigens in a sample can also be
CC   carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 675 BP; 150 A; 210 C; 186 G; 129 T; 0 U; 0 Other;

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 2.2e-75;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||  ||||||  |||||||| ||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||  |||||    | |  ||||  ||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||  ||  |||||  |  |||||||||   ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||  | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | |||  ||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 7
AAH41657
ID   AAH41657 standard; DNA; 675 BP.
XX
AC   AAH41657;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Human interleukin 8 antibody nucleotide sequence M1-5H.
XX
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033042.
XX
PR   06-DEC-1999;   99US-00456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding to
PT   nonhuman-antibodies, involves contacting sample with human antibody which
PT   binds to antibodies from nonhuman species and detecting binding.
XX
PS   Example 22; Page 87; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the amount
CC   of target antigen in a sample in a semi-quantitative or relative sense.
CC   Quantification of one or more target antigens in a sample can also be
CC   carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 675 BP; 150 A; 210 C; 186 G; 129 T; 0 U; 0 Other;

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 2.2e-75;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | |||||||||||||  ||||||  |||||||| ||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||  |||||    | |  ||||  ||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||  ||  |||||  |  |||||||||   ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              ||||||||||||||||||||||  ||||||||||||||||||||||||||||||  | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | |||  ||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
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```
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 8
AAH30003
ID   AAH30003 standard; DNA; 675 BP.
XX
AC   AAH30003;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody nucleotide fragment M1-5H.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027237.
XX
PR   02-OCT-1999;   99US-0157415P.
PR   01-DEC-1999;   99US-00453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS   Example 22; Page 91; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 675 BP; 150 A; 210 C; 186 G; 129 T; 0 U; 0 Other;

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 2.2e-75;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||   | | |||| ||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||| || ||||| | ||||||||  ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| |||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 9
AAH30019
ID   AAH30019 standard; DNA; 675 BP.
XX
AC   AAH30019;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody nucleotide fragment M2-11H.
XX
KW   Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW   human antibody phage display library; immunisation; transgenic animal;
KW   ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200125492-A1.
XX
PD   12-APR-2001.
XX
PF   02-OCT-2000; 2000WO-US027237.
XX
PR   02-OCT-1999;   99US-0157415P.
PR   01-DEC-1999;   99US-00453234.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-335567/35.
XX
PT   Producing a human antibody phage display library comprises providing a
PT   transgenic animal whose genome comprises human immunoglobulin genes and
PT   isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS   Example 22; Page 94-95; 161pp; English.
XX
CC   The present invention describes a method (M1) for producing a human
CC   antibody phage display library (I), comprising: (1) providing a nonhuman
CC   transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC   (2) isolating nucleic acids encoding human antibody chains (III) from
CC   lymphatic cells; and (3) forming a library of display packages whose
CC   members comprise a nucleic acid encoding (III) which is displayed from
CC   the package. The method is used for producing a human antibody display
CC   library, e.g., a Fab phage display library. The display method may be
CC   used to screen nucleic acids encoding antibody chains obtained from
CC   immunised nonhuman transgenic animals, and from this a population of
CC   antibodies may be prepared. Production of a human monoclonal antibodies
CC   display library using this method means there is no need to immunise
CC   humans with antigens, and the difficulties faced with immortalising B
CC   cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
```

```
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 675 BP; 150 A; 210 C; 186 G; 129 T; 0 U; 0 Other;

  Query Match            77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity  87.2%;  Pred. No. 2.2e-75;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| ||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 10
AAH41655
ID   AAH41655 standard; DNA; 677 BP.
XX
AC   AAH41655;
XX
DT   28-AUG-2001  (first entry)
XX
DE   Human interleukin 8 antibody nucleotide sequence M1-3H.
XX
KW   Human antibody; detection; Fab; immunoglobulin; heterophilic antibody;
KW   human anti-mouse antibody; HAMA antibody; interleukin 8; IL-8; Herpes;
KW   target antigen; bacterial; fungal; viral; pathogen; human disease;
KW   hepatitis A; hepatitis B; hepatitis C; influenza; Giardia; Malaria;
KW   Leishmania; Staphylococcus aureus; Pseudomonas aeruginosa; diagnosis; ds.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200140306-A1.
XX
PD   07-JUN-2001.
XX
PF   06-DEC-2000; 2000WO-US033042.
XX
PR   06-DEC-1999;   99US-00456090.
XX
PA   (BIOS-) BIOSITE DIAGNOSTICS INC.
PA   (GENP-) GENPHARM INT.
XX
PI   Buechler J,  Valkirs G,  Gray J,  Lonberg N;
XX
DR   WPI; 2001-374798/39.
XX
PT   Detecting analyte in human sample containing human antibodies binding to
PT   nonhuman-antibodies, involves contacting sample with human antibody which
PT   binds to antibodies from nonhuman species and detecting binding.
XX
PS   Example 22; Page 87; 135pp; English.
XX
CC   The present invention describes a method for detecting an analyte in a
CC   human sample containing human antibodies that specifically bind to
CC   antibodies from a nonhuman species. The method involves contacting the
CC   sample with a human antibody (I) which specifically binds to antibodies
CC   from a nonhuman species and detecting the binding between (I) and the
CC   analyte to indicate presence of the analyte. The method is used for
CC   detecting an analyte in a human sample containing human anti-mouse
CC   antibody (HAMA) (preferably human anti-mouse idiotype antibodies and/or
CC   heterophilic antibodies). The method can also be used for detecting any
CC   type of target antigen including bacterial, fungal and viral pathogens
CC   that cause human diseases e.g., hepatitis (A,B and C), influenza, Herpes,
CC   Giardia, Malaria, Leishmania, Staphylococcus aureus, Pseudomonas
CC   aeruginosa. Human antibodies can be used as detection reagents for
CC   performing clinical diagnostic tests and for performing other in vitro
CC   detection assays, including for research purposes. (I) can be used in
CC   qualitative assays designed to indicate the presence of one or more
CC   target antigens above minimally detectable amounts of antigen in the
CC   sample that usually correspond to the sensitivity limitations of the
CC   assays for each target antigen. Also, (I) is used to determine the amount
CC   of target antigen in a sample in a semi-quantitative or relative sense.
CC   Quantification of one or more target antigens in a sample can also be
CC   carried out using (I). AAH41612 to AAH41686, and AAB99361 to AAB99399,
CC   represent sequences used in the exemplification of the present invention
XX
SQ   Sequence 677 BP; 150 A; 213 C; 185 G; 129 T; 0 U; 0 Other;

  Query Match            77.5%;  Score 288.2;  DB 4;  Length 677;
  Best Local Similarity  86.9%;  Pred. No. 3.3e-75;
  Matches  333;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              || |||||||||  |||||||||||| |||||| ||||||||| ||||||||||||||
Db          3 GATGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 62

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||
Db         63 TCCTGTGCAGCGTCTGGATTCACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCT 122

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||
Db        123 CCAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTAT 182

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 242

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG-- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        243 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGG 302

Qy        299 ----------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACC 348
                       | ||| |||||||||||||||||||||||||||||||||  |||||
Db        303 ATCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 362

Qy        349 AAGGCTCCGGATGTGTTCCCTCT 371
              ||||  ||    || ||||| ||
Db        363 AAGGGCCCATCGGTCTTCCCCCT 385


RESULT 11
AAH30001
ID   AAH30001 standard; DNA; 677 BP.
XX
AC   AAH30001;
XX
DT   19-JUL-2001  (first entry)
XX
DE   Anti-IL8 monoclonal antibody nucleotide fragment M1-3H.
XX
```

KW Human; antibody; immunoglobulin; interleukin 8; IL8; immunogen;
KW human antibody phage display library; immunisation; transgenic animal;
KW ds.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN WO200125492-A1.
XX
PD 12-APR-2001.
XX
PF 02-OCT-2000; 2000WO-US027237.
XX
PR 02-OCT-1999; 99US-0157415P.
PR 01-DEC-1999; 99US-00453234.
XX
PA (BIOS-) BIOSITE DIAGNOSTICS INC.
PA (GENP-) GENPHARM INT SUBSIDIARY OF MEDAREX INC.
XX
PI Buechler J, Valkirs G, Gray J, Lonberg N;
XX
DR WPI; 2001-335567/35.
XX
PT Producing a human antibody phage display library comprises providing a
PT transgenic animal whose genome comprises human immunoglobulin genes and
PT isolating nucleic acids encoding antibody chains from lymphatic cells.
XX
PS Example 22; Page 91; 161pp; English.
XX
CC The present invention describes a method (M1) for producing a human
CC antibody phage display library (I), comprising: (1) providing a nonhuman
CC transgenic animal (II) whose genome comprises human immunoglobulin genes;
CC (2) isolating nucleic acids encoding human antibody chains (III) from
CC lymphatic cells; and (3) forming a library of display packages whose
CC members comprise a nucleic acid encoding (III) which is displayed from
CC the package. The method is used for producing a human antibody display
CC library, e.g., a Fab phage display library. The display method may be
CC used to screen nucleic acids encoding antibody chains obtained from
CC immunised nonhuman transgenic animals, and from this a population of
CC antibodies may be prepared. Production of a human monoclonal antibodies
CC display library using this method means there is no need to immunise
CC humans with antigens, and the difficulties faced with immortalising B
CC cells are avoided. AAH29958 to AAH30066 and AAB74994 to AAB75056
CC represent sequences used in the exemplification of the present invention
XX
SQ Sequence 677 BP; 150 A; 213 C; 185 G; 129 T; 0 U; 0 Other;

Query Match 77.5%; Score 288.2; DB 4; Length 677;
Best Local Similarity 86.9%; Pred. No. 3.3e-75;
Matches 333; Conservative 0; Mismatches 38; Indels 12; Gaps 1;

```
Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              || ||||||||| |  |||||||||||| |||||| |||||||||| ||||||||||||||
Db          3 GATGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 62

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              |||||||||| ||||||||||||||   | | |||| |||||||||||||||||||||||
Db         63 TCCTGTGCAGCGTCTGGATTCACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCT 122

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||
Db        123 CCAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTAT 182

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 242

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG-- 298
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        243 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGG 302

Qy        299 ----------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACC 348
                       | ||| ||||||||||||||||||||||||||||||||||||  |||||
```

Db 303 ATCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 362

Qy 349 AAGGCTCCGGATGTGTTCCCTCT 371
|||| || || ||||| ||
Db 363 AAGGGCCCATCGGTCTTCCCCCT 385

RESULT 12
ADE28458
ID ADE28458 standard; cDNA; 1398 BP.
XX
AC ADE28458;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-CD40 antibody 23-28-1 variable region heavy chain cDNA.
XX
KW anti-CD40 monoclonal antibody; CD40; cytostatic; virucide; antibacterial;
KW immunostimulant; anti-HIV; hyperproliferative; cancer; viral;
KW bacterial infection; immunodeficiency; neutropenia; HIV; gene therapy;
KW human; variable region heavy chain; ss; gene; 23-28-1.
XX
OS Homo sapiens.
XX
PN WO2003040170-A2.
XX
PD 15-MAY-2003.
XX
PF 08-NOV-2002; 2002WO-US036107.
XX
PR 09-NOV-2001; 2001US-0348980P.
XX
PA (PFIZ) PFIZER PROD INC.
PA (ABGE-) ABGENIX INC.
XX
PI Bedian V, Gladue RP, Corvalan J, Jia X, Feng X;
XX
DR WPI; 2003-441521/41.
DR P-PSDB; ADE28459.
XX
PT New chimeric or human monoclonal antibody or its antigen-binding portion
PT that specifically binds to and activates human CD40, useful for enhancing
PT an immune response in a human, or treating cancer, HIV, neutropenia or
PT viral infections.
XX
PS Claim 24; SEQ ID NO 65; 177pp; English.
XX
CC The invention relates to a novel chimeric or human monoclonal antibody or
CC its antigen-binding portion that specifically binds to and activates
CC human CD40. The anti-CD40 antibody of the invention demonstrates
CC cytostatic, virucide, antibacterial, immunostimulant and anti-HIV
CC activities and may be useful for treating a hyperproliferative disorder
CC such as cancer, viral and bacterial infection or genetic, primary or
CC combined immunodeficiency conditions including neutropenia or HIV
CC infection. The anti-CD40 antibodies may also be useful for detecting CD40
CC in a biological sample in vitro or in vivo, as well as during gene
CC therapy procedures. The current sequence is that of the human anti-CD40
CC antibody variable region heavy chain cDNA of the invention.
XX
SQ Sequence 1398 BP; 317 A; 431 C; 391 G; 259 T; 0 U; 0 Other;

Query Match 77.4%; Score 287.8; DB 10; Length 1398;
Best Local Similarity 86.4%; Pred. No. 5.6e-75;
Matches 338; Conservative 0; Mismatches 32; Indels 21; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |   |||| ||||||||||||||||||||||
Db        119 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGTCATGCACTGGGTCCGCCAGGCTC 178
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Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATGTCATATGATGGAAGTAGTAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        239 CAAACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              ||||||| |||||||||||||||||||||||||||||||||||||||| | | |  |
Db        299 TGCAAATAAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGG 358

Qy        302 G--------------------CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 340
              |                    |||||||||||||||| ||||||||||||||||||||
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Qy        341 CACCCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCTCCACCAAGGGCCCATCGGTCTTCCCCCT 449


RESULT 13
AAA46870
ID   AAA46870 standard; DNA; 1392 BP.
XX
AC   AAA46870;
XX
DT   03-OCT-2000  (first entry)
XX
DE   DNA encoding the heavy chain of immunoglobulin clone 6.1.1.
XX
KW   Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW   hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW   proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1392
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XX
PN   WO200037504-A2.
XX
PD   29-JUN-2000.
XX
PF   23-DEC-1999;   99WO-US030895.
XX
PR   23-DEC-1998;   98US-0113647P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Hanson DC,  Neveu MJ,  Mueller EE,  Hanke JH,  Gilman SC,  Davis CG;
PI   Corvalan JR;
XX
DR   WPI; 2000-442647/38.
DR   P-PSDB; AAY93707.
XX
PT   Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT   -4 containing specified heavy and light chain sequences, useful for
PT   treating, e.g. immune disorders.
XX
PS   Example 2; Fig 1D; 157pp; English.
XX
CC   The present sequence encodes a heavy chain of an antibody of the
CC   invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC   -4. Antibodies of the invention are composed of a heavy chain variable
CC   region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC   encoded by a human VH3-33 family gene. The modifications are contained in
CC   CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC   inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC   disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC   proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC   used to up-regulate immune system to up-regulate immunodeficient
CC   disorders
XX
SQ   Sequence 1392 BP; 314 A; 432 C; 391 G; 255 T; 0 U; 0 Other;

  Query Match             77.3%;  Score 287.4;  DB 3;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 7.3e-75;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | ||||| ||||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
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Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 14
AAA46896
ID   AAA46896 standard; DNA; 1392 BP.
XX
AC   AAA46896;
XX
DT   03-OCT-2000  (first entry)
XX
DE   DNA encoding the heavy chain of immunoglobulin clone 6.1.1.
XX
KW   Cytotoxic T-lymphocyte antigen-4; CTLA-4; antibody; immune system;
KW   hyperimmunity disorder; autoimmune disease; diabetes; graft rejection;
KW   proliferative disorder; cancer; immunodeficient disorder; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT   sig_peptide     1. .57
FT                   /*tag=  b
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PN   WO200037504-A2.
XX
PD   29-JUN-2000.
XX
PF   23-DEC-1999;   99WO-US030895.
XX
PR   23-DEC-1998;   98US-0113647P.
XX
PA   (PFIZ ) PFIZER INC.
PA   (ABGE-) ABGENIX INC.
XX
PI   Hanson DC,  Neveu MJ,  Mueller EE,  Hanke JH,  Gilman SC,  Davis CG;
PI   Corvalan JR;
```

```
XX
DR   WPI; 2000-442647/38.
DR   P-PSDB; AAY93732.
XX
PT   Novel antibodies capable of binding cytotoxic T-lymphocyte antigen (CTLA)
PT   -4 containing specified heavy and light chain sequences, useful for
PT   treating, e.g. immune disorders.
XX
PS   Example 2; Fig 221; 157pp; English.
XX
CC   The present sequence encodes a heavy chain of an antibody of the
CC   invention. The antibody is directed cytotoxic T-lymphocyte antigen (CTLA)
CC   -4. Antibodies of the invention are composed of a heavy chain variable
CC   region, comprising a modified contiguous sequence from a FR1-FR3 sequence
CC   encoded by a human VH3-33 family gene. The modifications are contained in
CC   CDR1, CDR2 and/or framework regions. The antibodies may be used to
CC   inhibit CTLA-4 and down-regulate the immune system to treat hyperimmunity
CC   disorders (e.g. autoimmune disease, diabetes and graft rejection) and
CC   proliferative disorders (e.g. cancer). CTLA-4 stimulatory agents may be
CC   used to up-regulate immune system to up-regulate immunodeficient
CC   disorders
XX
SQ   Sequence 1392 BP; 314 A; 432 C; 391 G; 255 T; 0 U; 0 Other;

  Query Match             77.3%;  Score 287.4;  DB 3;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 7.3e-75;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||  |||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | ||||| ||||||||||||||||||||||||
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Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | |||||||||||||||||||||||||||||||||||||||  |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 15
AAD54347
ID   AAD54347 standard; cDNA; 1392 BP.
XX
AC   AAD54347;
XX
DT   17-JUN-2003  (first entry)
XX
DE   Human 6.1.1 anti-CTLA-4 antibody heavy chain cDNA.
XX
KW   Human; cytotoxic T lymphocyte antigen-4; therapy; CTLA-4 antibody;
KW   cancer; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /product= "Anti-CTLA-4 antibody heavy chain"
FT   sig_peptide     1. .57
FT                   /*tag=  b
FT   mat_peptide     58. .1389
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FT                   /product= "Mature anti-CTLA-4 antibody heavy chain"
XX
PN   EP1262193-A1.
XX
PD   04-DEC-2002.
XX
PF   23-MAY-2002; 2002EP-00253652.
XX
PR   23-MAY-2001; 2001US-0293042P.
XX
PA   (PFIZ ) PFIZER PROD INC.
XX
PI   Hanson DC,  Mueller EE;
XX
DR   WPI; 2003-131215/13.
DR   P-PSDB; AAE35887.
XX
PT   Use of human anti-cytotoxic T lymphocyte antigen-4 antibody in the
PT   preparation of medicament for the treatment of cancer.
XX
PS   Disclosure; Fig 1L; 76pp; English.
XX
CC   The invention relates to the use of human anti-cytotoxic T lymphocyte
CC   antigen-4 (anti-CTLA-4) antibody in the preparation of a medicament for
CC   the treatment of cancer such as bone cancer, pancreatic cancer, skin
CC   cancer, cutaneous or intraocular malignant melanoma, uterine and ovarian
CC   cancer, cancer of the anal region, stomach cancer, breast cancer,
CC   testicular cancer, uterine cancer and carcinoma of the fallopian tubes.
CC   The present sequence is human anti-CTLA-4 antibody heavy chain cDNA
XX
SQ   Sequence 1392 BP; 314 A; 432 C; 391 G; 255 T; 0 U; 0 Other;

  Query Match             77.3%;  Score 287.4;  DB 10;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 7.3e-75;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||  |||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
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Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	290.4	78.1	675	4	US-09-456-090A-67	Sequence 67, Appl
2	290.4	78.1	675	4	US-09-453-234-67	Sequence 67, Appl
3	288.8	77.6	675	4	US-09-456-090A-59	Sequence 59, Appl
4	288.8	77.6	675	4	US-09-456-090A-91	Sequence 91, Appl
5	288.8	77.6	675	4	US-09-453-234-59	Sequence 59, Appl
6	288.8	77.6	675	4	US-09-453-234-91	Sequence 91, Appl
7	288.2	77.5	677	4	US-09-456-090A-55	Sequence 55, Appl
8	288.2	77.5	677	4	US-09-453-234-55	Sequence 55, Appl
9	287.4	77.3	1392	4	US-09-472-087-30	Sequence 30, Appl
10	287.4	77.3	1392	4	US-09-472-087-59	Sequence 59, Appl
11	287.2	77.2	675	4	US-09-456-090A-101	Sequence 101, App
12	287.2	77.2	675	4	US-09-453-234-101	Sequence 101, App
13	286	76.9	1395	4	US-09-472-087-28	Sequence 28, Appl
14	286	76.9	1395	4	US-09-472-087-57	Sequence 57, Appl
15	285.8	76.8	1392	4	US-09-472-087-27	Sequence 27, Appl
16	285.8	76.8	1392	4	US-09-472-087-53	Sequence 53, Appl
17	285.8	76.8	1392	4	US-09-472-087-55	Sequence 55, Appl
18	284.2	76.4	1999	4	US-09-472-087-54	Sequence 54, Appl
19	284	76.3	675	4	US-09-456-090A-107	Sequence 107, App
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22	282.4	75.9	675	4	US-09-456-090A-105	Sequence 105, App
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27	281.8	75.8	675	4	US-09-456-090A-93	Sequence 93, Appl
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45	272.8	73.3	512	3	US-08-545-809A-30	Sequence 30, Appl

ALIGNMENTS

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RESULT 1
US-09-456-090A-67
; Sequence 67, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M1-23H
US-09-456-090A-67

  Query Match             78.1%;  Score 290.4;  DB 4;  Length 675;
  Best Local Similarity   87.4%;  Pred. No. 1.6e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
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Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
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                    | ||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 2
US-09-453-234-67
; Sequence 67, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-23H
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
US-09-453-234-67

  Query Match             78.1%;  Score 290.4;  DB 4;  Length 675;
  Best Local Similarity   87.4%;  Pred. No. 1.6e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  |  ||||||||||||| |||||| |||||||||  ||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||| | |||| |||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 3
US-09-456-090A-59
; Sequence 59, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M1-5H
US-09-456-090A-59

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 5.4e-85;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  |  ||||||||||||| |||||| |||||||||  ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||||||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 4
US-09-456-090A-91
; Sequence 91, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
;   LENGTH: 675
;   TYPE: DNA
```

```
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M2-11H
US-09-456-090A-91

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 5.4e-85;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||| || ||||| | |||||||||  |||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| ||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 5
US-09-453-234-59
; Sequence 59, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-5H
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
US-09-453-234-59

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 5.4e-85;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||| || ||||| | |||||||||  |||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| ||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 6
US-09-453-234-91
; Sequence 91, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M2-11H
US-09-453-234-91

  Query Match             77.6%;  Score 288.8;  DB 4;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 5.4e-85;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||| || ||||| | |||||||||  |||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181
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Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| ||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 7
US-09-456-090A-55
; Sequence 55, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 677
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (3)..(677)
;   OTHER INFORMATION: M1-3H
US-09-456-090A-55

  Query Match             77.5%;  Score 288.2;  DB 4;  Length 677;
  Best Local Similarity   86.9%;  Pred. No. 8.6e-85;
  Matches  333;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              || |||||||||  |  |||||||||||| |||||| ||||||||| ||||||||||||||
Db          3 GATGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 62

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||
Db         63 TCCTGTGCAGCGTCTGGATTCACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCT 122

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||
Db        123 CCAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTAT 182

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 242

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG-- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        243 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGG 302

Qy        299 ----------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACC 348
                     | ||| ||||||||||||||||||||||||||||||||||||  |||||
Db        303 ATCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 362

Qy        349 AAGGCTCCGGATGTGTTCCCTCT 371
              ||||  ||    || ||||| ||
Db        363 AAGGGCCCATCGGTCTTCCCCCT 385


RESULT 8
US-09-453-234-55
; Sequence 55, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 677
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-3H
;   NAME/KEY: CDS
;   LOCATION: (3)..(677)
US-09-453-234-55

  Query Match             77.5%;  Score 288.2;  DB 4;  Length 677;
  Best Local Similarity   86.9%;  Pred. No. 8.6e-85;
  Matches  333;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              || |||||||||  |  |||||||||||| |||||| ||||||||| ||||||||||||||
Db          3 GATGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 62

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||
Db         63 TCCTGTGCAGCGTCTGGATTCACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCT 122

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||
Db        123 CCAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTAT 182

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 242

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG-- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        243 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGG 302

Qy        299 ----------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACC 348
                     | ||| ||||||||||||||||||||||||||||||||||||  |||||
Db        303 ATCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 362

Qy        349 AAGGCTCCGGATGTGTTCCCTCT 371
              ||||  ||    || ||||| ||
Db        363 AAGGGCCCATCGGTCTTCCCCCT 385


RESULT 9
US-09-472-087-30
; Sequence 30, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
```

```
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-30

  Query Match             77.3%;  Score 287.4;  DB 4;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-84;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||  ||||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | ||||| ||||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| |   | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||   |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 10
US-09-472-087-59
; Sequence 59, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-59

  Query Match             77.3%;  Score 287.4;  DB 4;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 2.2e-84;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||  ||||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | ||||| ||||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| |   | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||   |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 11
US-09-456-090A-101
; Sequence 101, Application US/09456090A
; Patent No. 6680209
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  TITLE OF INVENTION: HUMAN ANTIBODIES AS DIAGNOSTIC REAGENTS
;  FILE REFERENCE: 020015-000200US
;  CURRENT APPLICATION NUMBER: US/09/456,090A
;  CURRENT FILING DATE:  1999-12-06
;  NUMBER OF SEQ ID NOS: 110
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M2-31H
US-09-456-090A-101

  Query Match             77.2%;  Score 287.2;  DB 4;  Length 675;
  Best Local Similarity   86.9%;  Pred. No. 1.8e-84;
  Matches  332;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||||||||| ||||||||| ||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGTCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||| ||    | | ||||   || ||||||||||||||| ||
Db         62 CCTGTGCAGCCTCTGGATTCACGTTCAGTTACTATGGTATACACTGGGTCCGCCAGGTTC 121
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Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||| || |||||||||||| |||||||||| ||||||| |||||||||||| |
Db        122 CAGGCAAGGGACTAGAGTGGGTGGCACTTATATCATACGATGGAAGCAATAAATACTACG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACTCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA------- 294
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGACTGGA 301

Qy        295 -----AAGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                  |    | ||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
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Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 12
US-09-453-234-101
; Sequence 101, Application US/09453234
; Patent No. 6794132
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M2-31H
US-09-453-234-101

  Query Match             77.2%;  Score 287.2;  DB 4;  Length 675;
  Best Local Similarity   86.9%;  Pred. No. 1.8e-84;
  Matches  332;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||||||||| |||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGTCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||| ||   | | ||||  || ||||||||||||||| ||
Db         62 CCTGTGCAGCCTCTGGATTCACGTTCAGTTACTATGGTATACACTGGGTCCGCCAGGTTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||| || |||||||||||| |||||||| ||||||| |||||||||||| |
Db        122 CAGGCAAGGGACTAGAGTGGGTGGCACTTATATCATACGATGGAAGCAATAAATACTACG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACTCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA------- 294
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGACTGGA 301

Qy        295 -----AAGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                  |    | ||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 13
US-09-472-087-28
; Sequence 28, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-28

  Query Match             76.9%;  Score 286;  DB 4;  Length 1395;
  Best Local Similarity   86.3%;  Pred. No. 6.4e-84;
  Matches  335;  Conservative    0;  Mismatches   35;  Indels   18;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | ||||||||||||| |||||| ||||||||| ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | | |||| |||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||  |||||||||||||||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        239 GAGACTCCGTGAAGGGCCGATTCACCATCTCCAGTGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGA-- 299
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |    ||
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGAGA 358

Qy        300 ----------------AGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCAC 343
                              | |||||||||||||||||||||||||||||||||||||||||
Db        359 GACTGGGGTCCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCT 418

Qy        344 CCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCACCAAGGGCCCATCGGTCTTCCCCCT 446


RESULT 14
US-09-472-087-57
; Sequence 57, Application US/09472087
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; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
;   LENGTH: 1395
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-57

  Query Match             76.9%;  Score 286;  DB 4;  Length 1395;
  Best Local Similarity   86.3%;  Pred. No. 6.4e-84;
  Matches  335;  Conservative    0;  Mismatches   35;  Indels   18;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| |||||||||||||    | | |||| ||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||  |||||||||||||||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGTAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGA-- 299
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Qy        300 ----------------AGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCAC 343
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Qy        344 CCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCACCAAGGGCCCATCGGTCTTCCCCCT 446


RESULT 15
US-09-472-087-27
; Sequence 27, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-27

  Query Match             76.8%;  Score 285.8;  DB 4;  Length 1392;
  Best Local Similarity   86.5%;  Pred. No. 7.5e-84;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||| ||| |||||||||||||||    |     ||| |||||||||||||||||||||||
Db        119 CCTGTGTAGCGTCTGGATTCACCTTCAGTAGCCATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||  |||||||||| ||||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGAAATAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTTTC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||| |||||||||||||||||||||||||||||| |   |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGGAGGTC 358

Qy        299 ------------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                          | |||||||||||||||||||||||||||||||||||||||  |||
Db        359 ACTTCGGTCCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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(without alignments)
6393.344 Million cell updates/sec

Title: US-09-403-107-145
Perfect score: 372
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	302.2	81.2	729	16	US-10-406-830-20	Sequence 20, Appl
3	294.8	79.2	396	15	US-10-309-764-54	Sequence 54, Appl
4	290.4	78.1	675	10	US-09-453-234-67	Sequence 67, Appl
5	290.2	78.0	342	18	US-10-738-120-9	Sequence 9, Appli
6	288.8	77.6	675	10	US-09-453-234-59	Sequence 59, Appl
7	288.8	77.6	675	10	US-09-453-234-91	Sequence 91, Appl
8	288.2	77.5	677	10	US-09-453-234-55	Sequence 55, Appl
9	287.8	77.4	1398	15	US-10-292-088-37	Sequence 37, Appl
10	287.4	77.3	1392	14	US-10-153-382-12	Sequence 12, Appl
11	287.4	77.3	1392	18	US-10-612-497-30	Sequence 30, Appl
12	287.4	77.3	1392	18	US-10-612-497-59	Sequence 59, Appl
13	287.4	77.3	1392	18	US-10-776-649-30	Sequence 30, Appl
14	287.4	77.3	1392	18	US-10-776-649-59	Sequence 59, Appl
15	287.2	77.2	675	10	US-09-453-234-101	Sequence 101, App
16	286.4	77.0	660	10	US-09-791-153A-56	Sequence 56, Appl
17	286	76.9	1395	14	US-10-153-382-8	Sequence 8, Appli
18	286	76.9	1395	18	US-10-612-497-28	Sequence 28, Appl
19	286	76.9	1395	18	US-10-612-497-57	Sequence 57, Appl
20	286	76.9	1395	18	US-10-776-649-28	Sequence 28, Appl
21	286	76.9	1395	18	US-10-776-649-57	Sequence 57, Appl
22	285.8	76.8	1392	14	US-10-153-382-1	Sequence 1, Appli
23	285.8	76.8	1392	14	US-10-153-382-4	Sequence 4, Appli
24	285.8	76.8	1392	18	US-10-612-497-27	Sequence 27, Appl
25	285.8	76.8	1392	18	US-10-612-497-53	Sequence 53, Appl
26	285.8	76.8	1392	18	US-10-612-497-55	Sequence 55, Appl
27	285.8	76.8	1392	18	US-10-776-649-27	Sequence 27, Appl
28	285.8	76.8	1392	18	US-10-776-649-53	Sequence 53, Appl
29	285.8	76.8	1392	18	US-10-776-649-55	Sequence 55, Appl
30	284.8	76.6	414	15	US-10-325-694-143	Sequence 143, App
31	284.4	76.5	357	15	US-10-010-729-8	Sequence 8, Appli
32	284.2	76.4	1999	14	US-10-153-382-2	Sequence 2, Appli
33	284.2	76.4	1999	18	US-10-612-497-54	Sequence 54, Appl
34	284.2	76.4	1999	18	US-10-776-649-54	Sequence 54, Appl
35	284	76.3	675	10	US-09-453-234-107	Sequence 107, App
36	283.8	76.3	405	15	US-10-309-764-58	Sequence 58, Appl
37	282.4	75.9	675	10	US-09-453-234-99	Sequence 99, Appl
38	282.4	75.9	675	10	US-09-453-234-105	Sequence 105, App
39	282.4	75.9	675	10	US-09-453-234-109	Sequence 109, App
40	282	75.8	783	17	US-10-642-120-5	Sequence 5, Appli
41	282	75.8	783	17	US-10-642-060-5	Sequence 5, Appli
42	282	75.8	783	17	US-10-642-122-5	Sequence 5, Appli
43	282	75.8	783	17	US-10-642-124-5	Sequence 5, Appli
44	282	75.8	783	17	US-10-621-269-5	Sequence 5, Appli
45	282	75.8	783	17	US-10-620-850-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-10-325-694-145
; Sequence 145, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 145
; LENGTH: 372
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-145

Query Match 100.0%; Score 372; DB 15; Length 372;
Best Local Similarity 100.0%; Pred. No. 1.6e-113;
Matches 372; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA 300

Qy        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTCCGGAT 360

Qy        361 GTGTTCCCTCTA 372
                ||||||||||||
Db        361 GTGTTCCCTCTA 372


RESULT 2
US-10-406-830-20
; Sequence 20, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
;  APPLICANT: ADAMS, GREGORY P.
;  APPLICANT:  HORAK, EVA M.
;  APPLICANT:  WEINER, LOUIS M.
;  APPLICANT:  JAMES, MARKS D.
;  TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
;  TITLE OF INVENTION:  THEREOF
;  FILE REFERENCE: 407T-000410US
;  CURRENT APPLICATION NUMBER: US/10/406,830
;  CURRENT FILING DATE:  2003-04-04
;  PRIOR APPLICATION NUMBER: US 60/370,276
;  PRIOR FILING DATE: 2002-04-05
;  NUMBER OF SEQ ID NOS: 37
;  SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
;   LENGTH: 729
;   TYPE: DNA
;   ORGANISM: Artificial
;   FEATURE:
;   OTHER INFORMATION: Nucleic acid encoding single chain antibody.
US-10-406-830-20

  Query Match             81.2%;  Score 302.2;  DB 16;  Length 729;
  Best Local Similarity   93.2%;  Pred. No. 3.9e-90;
  Matches  316;  Conservative    0;  Mismatches   23;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||||
Db          8 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 67

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||||
Db         68 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 127

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        128 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 187

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        188 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 247

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||  |
Db        248 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGAGTATTACTGTGCGAAGTATCCTT 307

Qy        302 GCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 340
                  |||||||||||||||||||||||||||||||||||
Db        308 TAAACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 346


RESULT 3
US-10-309-764-54
; Sequence 54, Application US/10309764
; Publication No. US20030232009A1
; GENERAL INFORMATION:
;  APPLICANT: Foltz, Ian
;  APPLICANT:  Babcook, John
;  APPLICANT:  Palathumpat, Raju
;  APPLICANT:  Yang, Xiao-dong
;  APPLICANT:  King, Chadwick T.
;  TITLE OF INVENTION: ANTI-CDR45RB ANTIBODIES FOR USE IN
;  TITLE OF INVENTION:  TREATING AUTOIMMUNE DISEASE AND TRANSPLANT REJECTION
;  FILE REFERENCE: ABGENIX.029A
;  CURRENT APPLICATION NUMBER: US/10/309,764
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337,276
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 54
;   LENGTH: 396
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-764-54

  Query Match             79.2%;  Score 294.8;  DB 15;  Length 396;
  Best Local Similarity   92.0%;  Pred. No. 9.2e-88;
  Matches  311;  Conservative    0;  Mismatches   27;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| |||||| ||||||||| ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||||
Db        119 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||||  ||||||||||||||| | || |||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCTGTTATATGGTATGATGGAAGTAAGAGATTCTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGGCTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              |||||||||||||||||||||||| |||||||||||||||||||||||||| ||    ||
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAACTACAG 358

Qy        302 GCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCA 339
                  |||||||||||||||||| ||||||||||||||||
Db        359 ACTACTGGGGCCAGGGAACCATGGTCACCGTCTCCTCA 396


RESULT 4
US-09-453-234-67
; Sequence 67, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
```

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;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-23H
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
US-09-453-234-67

  Query Match             78.1%;  Score 290.4;  DB 10;  Length 675;
  Best Local Similarity   87.4%;  Pred. No. 3.3e-86;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| ||||||||||||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| |||||  |||||||||||||| | |||| |||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGCTATATGGTATGATGGAAGTAAAACATACAATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||| |||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TAGGCTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 5
US-10-738-120-9
; Sequence 9, Application US/10738120
; Publication No. US20040208873A1
; GENERAL INFORMATION:
;  APPLICANT: Teeling, Jessica
;  APPLICANT:  Parren, Paul
;  APPLICANT:  Baadsgaard, Ole
;  APPLICANT:  Hudson, Debra
;  APPLICANT:  Petersen, Jorgen
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST INTERLEUKIN 8 (IL-8)
;  FILE REFERENCE: MXI-278
;  CURRENT APPLICATION NUMBER: US/10/738,120
;  CURRENT FILING DATE:  2003-12-16
;  PRIOR APPLICATION NUMBER: 60/433,728
;  PRIOR FILING DATE: 2002-12-16
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
;   LENGTH: 342
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-738-120-9

  Query Match             78.0%;  Score 290.2;  DB 18;  Length 342;
  Best Local Similarity   92.7%;  Pred. No. 3e-86;
  Matches  316;  Conservative    0;  Mismatches   23;  Indels    2;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||||||||    |  |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGC--GAAAAAGGA 299
              |||||||||||||||||||||||| |||||||||||||||||||||||  || | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGATACTT 301

Qy        300 AGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 340
              | ||||||||||||||||||||||||||||||||||||||
Db        302 TGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 342


RESULT 6
US-09-453-234-59
; Sequence 59, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-5H
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
US-09-453-234-59

  Query Match             77.6%;  Score 288.8;  DB 10;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 1.1e-85;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
```

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Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| ||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 7
US-09-453-234-91
; Sequence 91, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 91
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M2-11H
US-09-453-234-91

  Query Match             77.6%;  Score 288.8;  DB 10;  Length 675;
  Best Local Similarity   87.2%;  Pred. No. 1.1e-85;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||| |||||| ||||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||| |||||||| |||||    | | |||| ||||||||||||||||||||||||
Db         62 CCTGTGCAGCGTCTGGATTTACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||||
Db        122 CAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTATG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG--- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        242 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGGA 301

Qy        299 ---------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                      | ||| ||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


RESULT 8
US-09-453-234-55
; Sequence 55, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 55
;   LENGTH: 677
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: M1-3H
;   NAME/KEY: CDS
;   LOCATION: (3)..(677)
US-09-453-234-55

  Query Match             77.5%;  Score 288.2;  DB 10;  Length 677;
  Best Local Similarity   86.9%;  Pred. No. 1.8e-85;
  Matches  333;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              || ||||||||| |  |||||||||||| |||||| ||||||||| ||||||||||||||
Db          3 GATGTGCAGCTGGTGCAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTC 62

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              |||||||||||  |||||||||||||    | | |||| ||||||||||||||||||||||
Db         63 TCCTGTGCAGCGTCTGGATTCACCTTCAGTTACTATGGCATGCACTGGGTCCGCCAGGCT 122

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              |||||||||||||||||||||| || ||||| | |||||||||  ||||||||||||||
Db        123 CCAGGCAAGGGGCTGGAGTGGGTGACACTTATAACCTATGATGGAGATAATAAATACTAT 182

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 242

Qy        241 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAAAAAGG-- 298
              |||||||||||||||||||| |||||||||||||||||||||||||||||| | | |
Db        243 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGACGGG 302

Qy        299 ----------AAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACC 348
                       | ||| ||||||||||||||||||||||||||||||||||||  |||||
Db        303 ATCGGGTACTTTGACTATTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACC 362

Qy        349 AAGGCTCCGGATGTGTTCCCTCT 371
              ||||  ||    || ||||| ||
Db        363 AAGGGCCCATCGGTCTTCCCCCT 385


RESULT 9
US-10-292-088-37
; Sequence 37, Application US/10292088
; Publication No. US20030211100A1
; GENERAL INFORMATION:
;  APPLICANT: BEDIAN, VAHE
;  APPLICANT:  GLADUE, RONALD P.
;  APPLICANT:  CORVALAN, JOSE
```

```
;  APPLICANT:  JIA, XIAO-CHI
;  APPLICANT:  FENG, XIAO
;  TITLE OF INVENTION: ANTIBODIES TO CD40
;  FILE REFERENCE: ABX-PF/3 US
;  CURRENT APPLICATION NUMBER: US/10/292,088
;  CURRENT FILING DATE:  2003-03-14
;  PRIOR APPLICATION NUMBER: 60/348,980
;  PRIOR FILING DATE: 2001-11-09
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 37
;   LENGTH: 1398
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-292-088-37

  Query Match            77.4%;  Score 287.8;  DB 15;  Length 1398;
  Best Local Similarity   86.4%;  Pred. No. 3.1e-85;
  Matches  338;  Conservative    0;  Mismatches   32;  Indels   21;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||| ||||||  |||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |   |||| ||||||||||||||||||||||||
Db        119 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGTCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATGTCATATGATGGAAGTAGTAAATACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAAACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAAG 301
              ||||||| |||||||||||||||||||||||||||||||||||||||| | | | | |
Db        299 TGCAAATAAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGATGGGG 358

Qy        302 G--------------------CTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAG 340
              |                    |||||||||||||||| ||||||||||||||||||||
Db        359 GTAAAGCAGTGCCTGGTCCTGACTACTGGGGCCAGGGAATCCTGGTCACCGTCTCCTCAG 418

Qy        341 CACCCACCAAGGCTCCGGATGTGTTCCCTCT 371
              |  |||||||||  ||    || ||||| ||
Db        419 CCTCCACCAAGGGCCCATCGGTCTTCCCCCT 449


RESULT 10
US-10-153-382-12
; Sequence 12, Application US/10153382
; Publication No. US20030086930A1
; GENERAL INFORMATION:
;  APPLICANT: PFIZER PRODUCTS INC.
;  TITLE OF INVENTION: USES OF ANTI-CTLA-4 ANTIBODIES
;  FILE REFERENCE: PC23019A
;  CURRENT APPLICATION NUMBER: US/10/153,382
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 60/293042
;  PRIOR FILING DATE: 2001-05-23
;  NUMBER OF SEQ ID NOS: 39
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-153-382-12

  Query Match            77.3%;  Score 287.4;  DB 14;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 4.2e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||| ||||||  |||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |   |||| ||||||||||||||||||||||||
Db        119 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGTCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||| ||||||||||||||| ||||||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||||||| ||||||||||||||||||||||||||||||| |  | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||  |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 11
US-10-612-497-30
; Sequence 30, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV1
;  CURRENT APPLICATION NUMBER: US/10/612,497
;  CURRENT FILING DATE:  2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-612-497-30

  Query Match            77.3%;  Score 287.4;  DB 18;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 4.2e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  | ||||||||||||| ||||||  |||||||| ||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||  |||| ||||||||||||||    |  ||||| ||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||| ||||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238
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Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| |   | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||||  |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 12
US-10-612-497-59
; Sequence 59, Application US/10612497
; Publication No. US20040228858A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV1
;  CURRENT APPLICATION NUMBER: US/10/612,497
;  CURRENT FILING DATE:  2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-612-497-59

  Query Match            77.3%;  Score 287.4;  DB 18;  Length 1392;
  Best Local Similarity  86.8%;  Pred. No. 4.2e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||| ||||||  |||||||| ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    |  ||||| ||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| |   | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||||  |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 13
US-10-776-649-30
; Sequence 30, Application US/10776649
; Publication No. US20040228861A1
; GENERAL INFORMATION:
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV2
;  CURRENT APPLICATION NUMBER: US/10/776,649
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: US 10/612497
;  PRIOR FILING DATE: 2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-776-649-30

  Query Match            77.3%;  Score 287.4;  DB 18;  Length 1392;
  Best Local Similarity  86.8%;  Pred. No. 4.2e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||| ||||||  |||||||| ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    |  ||||| ||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||||||||| |   | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||||  |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 14
US-10-776-649-59
; Sequence 59, Application US/10776649
; Publication No. US20040228861A1
; GENERAL INFORMATION:
```

```
;  APPLICANT: Douglas C. Hanson
;  APPLICANT:  Mark J. Neveu
;  APPLICANT:  Eileen E. Mueller
;  APPLICANT:  Jeffrey H. Hanke
;  APPLICANT:  Steven C. Gilman
;  APPLICANT:  C. Geoffrey Davis
;  APPLICANT:  Jose R. Corvalan
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1 DIV2
;  CURRENT APPLICATION NUMBER: US/10/776,649
;  CURRENT FILING DATE:  2004-02-10
;  PRIOR APPLICATION NUMBER: US 10/612497
;  PRIOR FILING DATE: 2003-07-01
;  PRIOR APPLICATION NUMBER: US 09/472087
;  PRIOR FILING DATE: 1999-12-23
;  PRIOR APPLICATION NUMBER: US 60/113647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 59
;   LENGTH: 1392
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-776-649-59

  Query Match             77.3%;  Score 287.4;  DB 18;  Length 1392;
  Best Local Similarity   86.8%;  Pred. No. 4.2e-85;
  Matches  334;  Conservative    0;  Mismatches   36;  Indels   15;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||| ||||||  |||||||| ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCGAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||| |||| ||||||||||||||    | ||||| ||||||||||||||||||||||||
Db        119 CCTGTACAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||  |||||||||| |||||| ||||||
Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATGGTATGATGGAAGCAATAAACACTATG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        239 CAGACTCCGCGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||| |||||||||||||||||||||||||| | | | |
Db        299 TGCAAATGAACAGCCTGAGAGCCGAGGACACGGCTGTGTATTACTGTGCGAGAGCCGGAC 358

Qy        301 --------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                           | ||||||||||||||||||||||||||||||||||||||  |||
Db        359 TGCTGGGTTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCA 418

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        419 CCAAGGGCCCATCGGTCTTCCCCCT 443


RESULT 15
US-09-453-234-101
; Sequence 101, Application US/09453234
; Publication No. US20030091995A1
; GENERAL INFORMATION:
;  APPLICANT: Buechler, Joe
;  APPLICANT:  Valkirs, Gunars
;  APPLICANT:  Gray, Jeff
;  APPLICANT:  Lonberg, Nils
;  APPLICANT:  Biosite Diagnostics, Inc.
;  APPLICANT:  GenPharm International
;  TITLE OF INVENTION: Human Antibodies
;  FILE REFERENCE: 020015-000110US
;  CURRENT APPLICATION NUMBER: US/09/453,234
;  CURRENT FILING DATE:  1999-12-01
;  PRIOR APPLICATION NUMBER: US 60/157,415
;  PRIOR FILING DATE: 1999-10-02
;  NUMBER OF SEQ ID NOS: 112
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 101
;   LENGTH: 675
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(675)
;   OTHER INFORMATION: M2-31H
US-09-453-234-101

  Query Match             77.2%;  Score 287.2;  DB 10;  Length 675;
  Best Local Similarity   86.9%;  Pred. No. 3.8e-85;
  Matches  332;  Conservative    0;  Mismatches   38;  Indels   12;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||||||||| |||||||| ||||||||||||||||
Db          2 AGGTGCAGCTGGTGGAGTCTGGGGGAGTCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 61

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||| ||   | | ||||  || ||||||||||||||| ||
Db         62 CCTGTGCAGCCTCTGGATTCACGTTCAGTTACTATGGTATACACTGGGTCCGCCAGGTTC 121

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||| || |||||||||||| |||||||||| |||||||| |||||||||| |
Db        122 CAGGCAAGGGACTAGAGTGGGTGGCACTTATATCATACGATGGAAGCAATAAATACTACG 181

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||
Db        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACTCTGTATC 241

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA------- 294
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAGACTGGA 301

Qy        295 -----AAGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCA 349
                  |    | ||||||||||||||||||||||||||||||||||||||||  ||||||
Db        302 TCGGGTACTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCCTCCACCA 361

Qy        350 AGGCTCCGGATGTGTTCCCTCT 371
              |||  ||    || ||||| ||
Db        362 AGGGCCCATCGGTCTTCCCCCT 383


Search completed: December  7, 2004, 14:26:31
Job time : 320.733 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 ; Search time 2170.93 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-145
Perfect score: 372
Sequence: 1 gaggtgcagctgctcgagtc.....ctccggatgtgttccctcta 372

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	283.2	76.1	503	2	AW402572	AW402572 UI-HF-BK0
2	279.4	75.1	648	4	BG340670	BG340670 602462250
3	278	74.7	918	5	BQ710537	BQ710537 AGENCOURT
4	277.8	74.7	950	5	BQ708952	BQ708952 AGENCOURT
5	277	74.5	621	6	CD687626	CD687626 EST4147 h
6	276.8	74.4	907	5	BQ708724	BQ708724 AGENCOURT
7	276.8	74.4	1001	4	BM914366	BM914366 AGENCOURT
8	274.2	73.7	678	4	BG340648	BG340648 602462226
9	274.2	73.7	788	4	BG342203	BG342203 602462979
10	274.2	73.7	870	4	BG759649	BG759649 602713342
11	274.2	73.7	964	2	BF663281	BF663281 602144406
12	274.2	73.7	991	2	BF974524	BF974524 602243430
13	274.2	73.7	1010	2	BF663436	BF663436 602144593
14	273.2	73.4	846	4	BG755572	BG755572 602716255
15	272.6	73.3	912	4	BG756211	BG756211 602713521
16	272.6	73.3	930	4	BG755605	BG755605 602716292
17	271.8	73.1	413	5	BX344075	BX344075 BX344075
18	270.6	72.7	516	2	AW401728	AW401728 UI-HF-BK0
19	270	72.6	761	4	BG757080	BG757080 602715111
20	269.8	72.5	937	5	BQ706852	BQ706852 AGENCOURT
21	269.6	72.5	899	5	BQ420418	BQ420418 AGENCOURT
22	269.4	72.4	436	2	AW402311	AW402311 UI-HF-BK0
23	269.4	72.4	663	4	BG686759	BG686759 602650729
24	268.8	72.3	962	5	BQ706534	BQ706534 AGENCOURT
25	268.8	72.3	1000	5	BQ712690	BQ712690 AGENCOURT
26	268.2	72.1	999	5	BQ707443	BQ707443 AGENCOURT
27	267	71.8	891	5	BQ709554	BQ709554 AGENCOURT
28	267	71.8	986	5	BQ710656	BQ710656 AGENCOURT
29	266.8	71.7	894	5	BQ708235	BQ708235 AGENCOURT
30	266.6	71.7	456	4	BG503730	BG503730 602549705
31	266.6	71.7	902	5	BX436850	BX436850 BX436850
32	266.4	71.6	1228	4	BM920476	BM920476 AGENCOURT
33	265.8	71.5	413	5	BX399298	BX399298 BX399298
34	264.6	71.1	958	5	BQ709987	BQ709987 AGENCOURT
35	263.8	70.9	896	5	BQ717993	BQ717993 AGENCOURT
36	263.2	70.8	750	2	BF976111	BF976111 602244955
37	262.4	70.5	430	5	BX480277	BX480277 DKFZp686O
38	262.4	70.5	906	5	BU151579	BU151579 AGENCOURT
39	262.2	70.5	889	5	BQ709105	BQ709105 AGENCOURT
40	262.2	70.5	925	5	BQ706858	BQ706858 AGENCOURT
41	261.4	70.3	536	2	AW402624	AW402624 UI-HF-BK0
42	259.8	69.8	891	5	BU150876	BU150876 AGENCOURT
43	259.8	69.8	1007	4	BM914489	BM914489 AGENCOURT
44	258.6	69.5	802	4	BG756245	BG756245 602713557
45	258	69.4	870	5	BQ711138	BQ711138 AGENCOURT

ALIGNMENTS

RESULT 1
AW402572
LOCUS AW402572 503 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BK0-aax-b-12-0-UI.r1 NIH_MGC_36 Homo sapiens cDNA clone IMAGE:3055079 5', mRNA sequence.
ACCESSION AW402572
VERSION AW402572.1 GI:6921271
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 503)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .503
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3055079"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_36"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (0.5-1.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

Query Match 76.1%; Score 283.2; DB 2; Length 503;
Best Local Similarity 85.5%; Pred. No. 4.4e-73;

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  Matches  337;  Conservative    0;  Mismatches   33;  Indels   24;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | |||||||||||||| ||||||| |||||||||| ||||||||||||||||
Db         44 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 103

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |    ||||| ||||||||||||||||||||||
Db        104 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGCTATGCACTGGGTCCGCCAGGCTC 163

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||||||||||||||||||||| ||||||||| || |
Db        164 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAATAATAAATATTACG 223

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        224 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 283

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAA------ 295
              |||||||||||| |||||||||||||||||||||||||||||||||||| ||
Db        284 TGCAAATGAACAGACTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAGAACCCCAA 343

Qy        296 ------------------AGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT 337
                              |  ||||||||||||||||||||||||||||||||||||||||
Db        344 ATTACGATTTTTGGAGTGCCACAAACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT 403

Qy        338 CAGCACCCACCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||  |||||||||  ||    || ||||| ||
Db        404 CAGCTTCCACCAAGGGCCCATCGGTCTTCCCCCT 437


RESULT 2
BG340670
LOCUS       BG340670                 . 648 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602462250F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4574941 5',
            mRNA sequence.
ACCESSION   BG340670
VERSION     BG340670.1  GI:13147108
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 648)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1285  row: d  column: 14
            High quality sequence stop: 648.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4574941"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           75.1%;  Score 279.4;  DB 4;  Length 648;
  Best Local Similarity   86.3%;  Pred. No. 6.3e-72;
  Matches  322;  Conservative    0;  Mismatches   46;  Indels    5;  Gaps    1;

Qy          1 GAGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTC 60
              |||||||||||| | |||||||||||||| | ||||||||||||||||||||||||||||||
Db         82 GAGGTGCAGCTGTTGGAGTCTGGGGGAGGCTTGGTACAGCCTGGGGGGTCCCTGAGACTC 141

Qy         61 TCCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCT 120
              ||||||||||||||||||||||||||||      |||||||| ||||||||||||||||
Db        142 TCCTGTGCAGCCTCTGGATTCACCTTTAGCAGCTATGCCATGAGCTGGGTCCGCCAGGCT 201

Qy        121 CCAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTAT 180
              ||||| |||||||||||||||||  ||| |||       |  |||  |||  | ||||||
Db        202 CCAGGGAAGGGGCTGGAGTGGGTCTCAGCTATTAGTGGTAGTGGTGGTAGCACATACTAC 261

Qy        181 GCAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 240
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        262 GCAGACTCCGTGAAGGGCCGGTTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTAT 321

Qy        241 CTGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA---- 296
              |||||||||||||||||||||||| |||||||||| || ||||||||||||    |
Db        322 CTGCAAATGAACAGCCTGAGAGCCGAGGACACGGCCGTATATTACTGTGCGACCCACCCG 381

Qy        297 -GGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTC 355
               || ||||    ||| |  ||||||||||||||||||||||||||||||||||||||||
Db        382 GTGATGGCTGACTGGGGCCAGGAACCCTGGTCACCGTCTCCTCAGCACCCACCAAGGCTC 441

Qy        356 CGGATGTGTTCCC 368
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Db        442 CGGATGTGTTCCC 454


RESULT 3
BQ710537
LOCUS       BQ710537                 918 bp    mRNA    linear   EST 16-JUL-2002
DEFINITION  AGENCOURT_8354676 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6281052
            5', mRNA sequence.
ACCESSION   BQ710537
VERSION     BQ710537.1  GI:21849436
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 918)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Mark Watson
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2473  row: d  column: 13
            High quality sequence stop: 612.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:6281052"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
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/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.7%; Score 278; DB 5; Length 918;
Best Local Similarity 85.1%; Pred. No. 1.8e-71;
Matches 330; Conservative 0; Mismatches 40; Indels 18; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        126 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 185

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||||||||    |  |||||  |||||||||||||||||||||||
Db        186 CCTGTGCAGCGTCTGGATTCACCTTCAGTAGTTATGGCATGCACTGGGTCCGCCAGGCTC 245

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||||  |||||    | ||||||||  | ||||||||||||
Db        246 CAGGCAAGGGGCTGGAGTGGGTGGCATTTATACGGTTTGATGGAAATGATAAATACTATG 305

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAAGGAA- 300
              |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||| | | |
Db        366 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTACTACTGTGCGAAAGATGGAG 425

Qy        301 -----------------GGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCAC 343
                              | |  ||||||| | || |||  ||||||||||||||||||
Db        426 TGGTTATGATGTTCATGGACGTCTGGGGCAAAGGGACCACGGTCACCGTCTCCTCAGCCT 485

Qy        344 CCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        486 CCACCAAGGGCCCATCGGTCTTCCCCCT 513
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RESULT 4
BQ708952
LOCUS BQ708952 950 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8485030 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6301022 5', mRNA sequence.
ACCESSION BQ708952
VERSION BQ708952.1 GI:21847851
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 950)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2516 row: d column: 15
High quality sequence stop: 694.
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/clone="IMAGE:6301022"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.7%; Score 277.8; DB 5; Length 950;
Best Local Similarity 85.2%; Pred. No. 2e-71;
Matches 328; Conservative 0; Mismatches 42; Indels 15; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        127 AGGTGCAGTTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 186

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||  ||||||||||||||    | |  ||||  |||||||||||||||||||||||
Db        187 CCTGTGCAGCGTCTGGATTCACCTTCAGTAACTATGGCATGCACTGGGTCCGCCAGGCTC 246

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              |||||||||||||||||||||||||||  ||||    ||||||||| ||| ||||||||||
Db        247 CAGGCAAGGGGCTGGAGTGGGTGGCATTTATTCGGTATGATGGAACTAAAAAATACTATG 306

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              |||||||  ||| ||||||||||||||||||||||||| ||||||||||||||||||||||
Db        307 CAGACTCTCTGAGGGGCCGATTCACCATCTCCAGAGAGAATTCCAAGAACACGCTGTATC 366

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAA------- 294
              |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db        367 TGCAAATGAACAGCCTGAGAGGTGACGACACGGCTGTGTATTACTGTGCGAAAGATCTTT 426

Qy        295 --------AAGGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCTCAGCACCCA 346
                      |    | |||||||||||||| |||||||||||||||||||||  |||
Db        427 TTGCGGGTTACTTTGACTACTGGGGCCAGGGGACCCTGGTCACCGTCTCCTCAGCCTCCA 486

Qy        347 CCAAGGCTCCGGATGTGTTCCCTCT 371
              ||||||  ||    || ||||| ||
Db        487 CCAAGGGCCCATCGGTCTTCCCCCT 511
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RESULT 5
CD687626
LOCUS CD687626 621 bp mRNA linear EST 25-JUN-2003
DEFINITION EST4147 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD687626
VERSION CD687626.1 GI:32205644
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 621)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
source 1. .621

/organism="Homo sapiens"
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/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 74.5%; Score 277; DB 6; Length 621;
Best Local Similarity 84.4%; Pred. No. 3.2e-71;
Matches 335; Conservative 0; Mismatches 35; Indels 27; Gaps 1;

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Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||  |  |||||||||||||  ||||||  |||||||||  ||||||||||||||||
Db         59 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 118

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
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Db        119 CCTGTGCAGCCTCTGGATTCACCTTCAGTCGCTATGCCATGCACTGGGTCCGCCAGGCTC 178

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        179 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAGGTAATAAATATTACG 238

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        239 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTCTC 298

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA----- 296
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Db        299 TGCAAATGAACAGCCTGAGACCTGAGGACACGGCTATGTATTACTGTGCGAGAGATCGGA 358

Qy        297 ----------------------GGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCT 334
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Db        359 ATTCTTATGCTTCGGGGAGTTCTATTGACTACTGGGGCCAGGGAATCCTGGTCACCGTCT 418

Qy        335 CCTCAGCACCCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        419 CCTCAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT 455
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RESULT 6
BQ708724
LOCUS BQ708724 907 bp mRNA linear EST 16-JUL-2002
DEFINITION AGENCOURT_8347234 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:6279099 5', mRNA sequence.
ACCESSION BQ708724
VERSION BQ708724.1 GI:21847623
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 907)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2468 row: c column: 04
High quality sequence stop: 587.
FEATURES Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6279099"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_113"
/note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 74.4%; Score 276.8; DB 5; Length 907;
Best Local Similarity 84.5%; Pred. No. 4e-71;
Matches 333; Conservative 0; Mismatches 37; Indels 24; Gaps 1;

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Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
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Db        163 CCTGTGCAGCGTCTGGATTCACCTTCAGTACCTATGGCATGCACTGGGTCCGCCAGGCTC 222

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        223 CAGGCAAGGGGCTGGAGTGGGTGTCATTTATACGGTATGATGGAAGTAATAAATACTATG 282

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        283 CAGACTTCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 342

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA----- 296
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Db        343 TGCAAATGAACAGCCTGAAACCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATTGCA 402

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Qy        338 CAGCACCCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        463 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT 496
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RESULT 7
BM914366
LOCUS BM914366 1001 bp mRNA linear EST 12-MAR-2002
DEFINITION AGENCOURT_6615562 NIH_MGC_113 Homo sapiens cDNA clone IMAGE:5480035 5', mRNA sequence.
ACCESSION BM914366
VERSION BM914366.1 GI:19364745
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1001)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Mark Watson
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2002 row: d column: 20

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           High quality sequence stop: 674.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5480035"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_113"
                     /note="Organ: spleen; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming. Directionally cloned
                     into EcoRI/XhoI sites using the following 5' adaptor:
                     GGCACGAG(G). Library constructed by Ling Hong in the
                     laboratory of Gerald M. Rubin (University of California,
                     Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
                     Superscript II RT (Life Technologies). Note: this is a
                     NIH_MGC Library."
ORIGIN

  Query Match             74.4%;  Score 276.8;  DB 4;  Length 1001;
  Best Local Similarity   84.5%;  Pred. No. 4.1e-71;
  Matches  333;  Conservative    0;  Mismatches   37;  Indels   24;  Gaps    1;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        102 AGGTGCAGCTGGTGGAATCTGGGGGAGGCGTGGTCCAGCCTGGGGGGTCCCTGAGACTCT 161

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
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Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        222 CAGGCAAGGGGCTGGAGTGGGTGTCATTTATACGGTATGATGGAAGTAATAAATACTATG 281

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA----- 296
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Db        342 TGCAAATGAACAGCCTGAAACCTGAGGACACGGCTGTGTATTACTGTGCGAAAGATTGCA 401

Qy        297 -------------------GGAAGGCTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT 337
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Db        402 TGTGGGGTGATGATTGCTCTTTTGACTACTGGGGCCAGGGAACCCTGGTCACCGTCTCCT 461

Qy        338 CAGCACCCACCAAGGCTCCGGATGTGTTCCCTCT 371
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Db        462 CAGCCTCCACCAAGGGCCCATCGGTCTTCCCCCT 495


RESULT 8
BG340648
LOCUS       BG340648                678 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602462226F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4574935 5',
            mRNA sequence.
ACCESSION   BG340648
VERSION     BG340648.1  GI:13147086
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 678)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1285  row: d  column: 08
            High quality sequence stop: 666.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4574935"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.7%;  Score 274.2;  DB 4;  Length 678;
  Best Local Similarity   95.6%;  Pred. No. 2.2e-70;
  Matches  282;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |   |||| ||||||||||||||||||||||||
Db        190 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 249

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 309

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA 424


RESULT 9
BG342203
LOCUS       BG342203                788 bp    mRNA    linear   EST 27-FEB-2001
DEFINITION  602462979F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4575931 5',
            mRNA sequence.
ACCESSION   BG342203
VERSION     BG342203.1  GI:13148641
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
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           Clone distribution: MGC clone distribution information can be
           found through the I.M.A.G.E. Consortium/LLNL at:
           http://image.llnl.gov
           Plate: LLCM1287  row: m  column: 20
           High quality sequence stop: 687.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:4575931"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.7%;  Score 274.2;  DB 4;  Length 788;
  Best Local Similarity   95.6%;  Pred. No. 2.3e-70;
  Matches  282;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        129 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 188

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
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Db        189 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 248

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        309 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 368

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
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Db        369 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA 423


RESULT 10
BG759649
LOCUS       BG759649                870 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602713342F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853338 5',
            mRNA sequence.
ACCESSION   BG759649
VERSION     BG759649.1  GI:14070302
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 870)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1699  row: d  column: 11
            High quality sequence stop: 764.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4853338"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.7%;  Score 274.2;  DB 4;  Length 870;
  Best Local Similarity   95.6%;  Pred. No. 2.4e-70;
  Matches  282;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||||| | ||||||||||||| |||||| ||||||||| ||||||||||||||||
Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |  |||| ||||||||||||||||||||||||
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Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        250 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 309

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA 424


RESULT 11
BF663281
LOCUS       BF663281                964 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602144406F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297849 5',
            mRNA sequence.
ACCESSION   BF663281
VERSION     BF663281.1  GI:11937163
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 964)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
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            http://image.llnl.gov
            Plate: LLCM1152  row: k  column: 02
            High quality sequence stop: 693.
FEATURES              Location/Qualifiers
     source           1. .964
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4297849"
                      /tissue_type="primary B-cells from tonsils (cell line)"
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_48"
                      /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                      for average insert size 1.8kb. Library constructed by Ling
                      Hong in the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies).
                      Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.7%;  Score 274.2;  DB 2;  Length 964;
  Best Local Similarity   95.6%;  Pred. No. 2.4e-70;
  Matches  282;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
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Db        190 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 249

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Db        250 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 309

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA 424


RESULT 12
BF974524
LOCUS       BF974524                991 bp    mRNA    linear   EST 22-JAN-2001
DEFINITION  602243430F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4334719 5',
            mRNA sequence.
ACCESSION   BF974524
VERSION     BF974524.1  GI:12341739
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 991)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1204  row: k  column: 08
            High quality sequence stop: 688.
FEATURES              Location/Qualifiers
     source           1. .991
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4334719"
                      /tissue_type="primary B-cells from tonsils (cell line)".
                      /lab_host="DH10B (phage-resistant)"
                      /clone_lib="NIH_MGC_48"
                      /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                      Site_2: EcoRI; cDNA made by oligo-dT priming.
                      Directionally cloned into EcoRI/XhoI sites using the
                      following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                      for average insert size 1.8kb. Library constructed by Ling
                      Hong in the laboratory of Gerald M. Rubin (University of
                      California, Berkeley) using  ZAP-cDNA synthesis kit
                      (Stratagene) and Superscript II RT (Life Technologies).
                      Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.7%;  Score 274.2;  DB 2;  Length 991;
  Best Local Similarity   95.6%;  Pred. No. 2.4e-70;
  Matches  282;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||||
Db        190 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 249

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
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Db        370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA 424


RESULT 13
BF663436
LOCUS       BF663436                1010 bp    mRNA    linear   EST 21-DEC-2000
DEFINITION  602144593F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4297847 5',
            mRNA sequence.
ACCESSION   BF663436
VERSION     BF663436.1  GI:11937331
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1010)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1152  row: j  column: 24
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          High quality sequence stop: 695.
FEATURES             Location/Qualifiers
     source          1. .1010
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4297847"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.7%;  Score 274.2;  DB 2;  Length 1010;
  Best Local Similarity   95.6%;  Pred. No. 2.4e-70;
  Matches  282;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
              |||||||||| | |||||||||||| |||||| |||||||| ||||||||||||||||||
Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||||
Db        190 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 249

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 309

Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAGA 424


RESULT 14
BG755572
LOCUS       BG755572                 846 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602716255F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4856628 5',
            mRNA sequence.
ACCESSION   BG755572
VERSION     BG755572.1  GI:14066225
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 846)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1707  row: m  column: 13
            High quality sequence stop: 752.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4856628"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.4%;  Score 273.2;  DB 4;  Length 846;
  Best Local Similarity   95.6%;  Pred. No. 4.7e-70;
  Matches  281;  Conservative    0;  Mismatches   13;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        130 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 189

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              |||||||||||||||||||||||||    |    |||| ||||||||||||||||||||||||
Db        190 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGCTATGGCATGCACTGGGTCCGCCAGGCTC 249

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Db        310 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 369

Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAA 295
              |||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        370 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGACAA 423


RESULT 15
BG756211
LOCUS       BG756211                 912 bp    mRNA    linear   EST 15-MAY-2001
DEFINITION  602713521F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853837 5',
            mRNA sequence.
ACCESSION   BG756211
VERSION     BG756211.1  GI:14066864
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 912)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1700  row: i  column: 06
            High quality sequence stop: 889.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4853837"
                     /tissue_type="primary B-cells from tonsils (cell line)"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_48"
                     /note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected >500bp
                     for average insert size 1.8kb. Library constructed by Ling
                     Hong in the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             73.3%;  Score 272.6;  DB 4;  Length 912;
  Best Local Similarity   95.3%;  Pred. No. 7.1e-70;
  Matches  281;  Conservative    0;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          2 AGGTGCAGCTGCTCGAGTCTGGGGGAGTCGTGGTACAGCCTGGGGGGTCCCTGAGACTCT 61
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Db        121 AGGTGCAGCTGGTGGAGTCTGGGGGAGGCGTGGTCCAGCCTGGGAGGTCCCTGAGACTCT 180

Qy         62 CCTGTGCAGCCTCTGGATTCACCTTTGATGATTATGCCATGCACTGGGTCCGCCAGGCTC 121
              ||||||||||||||||||||||||    |  ||||| |||| ||||||||||||||||||
Db        181 CCTGTGCAGCCTCTGGATTCACCTTCAGTAGTTATGGCATGAACTGGGTCCGCCAGGCTC 240

Qy        122 CAGGCAAGGGGCTGGAGTGGGTGGCAGTTATATCATATGATGGAAGTAATAAATACTATG 181
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Qy        182 CAGACTCCGTGAAGGGCCGATTCACCATCTCCAGAGACAATTCCAAGAACACGCTGTATC 241
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Qy        242 TGCAAATGAACAGCCTGAGAGCTGAGGACACGGCTGTGTATTACTGTGCGAAAAA 296
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Job time : 2171.93 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 02:37:53 ; Search time 1815.78 Seconds
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8360.047 Million cell updates/sec

Title: US-09-403-107-147
Perfect score: 321
Sequence: 1 gagctccagatgacccagtc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: gb_htg:*
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6: gb_pat:*
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8: gb_pl:*
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12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	6	A84380	A84380 Sequence 14
2	321	100.0	321	6	BD075296	BD075296 Novel met
3	321	100.0	1630	6	BD222938	BD222938 Heteromin
4	321	100.0	1630	6	BD222939	BD222939 Heteromin
5	321	100.0	1630	6	AX023365	AX023365 Sequence
6	321	100.0	1630	6	AX023367	AX023367 Sequence
7	260.2	81.1	321	6	A84374	A84374 Sequence 14
8	260.2	81.1	321	6	AX003761	AX003761 Sequence
9	260.2	81.1	321	6	BD075293	BD075293 Novel met
10	260.2	81.1	321	6	BD139668	BD139668 A novel m
11	245.8	76.6	324	6	BD187178	BD187178 Human-typ
12	245.8	76.6	324	6	BD187179	BD187179 Human-typ
13	244.2	76.1	339	9	AB006842	AB006842 Homo sapi
14	244.2	76.1	342	6	BD097614	BD097614 Antibody
15	242.6	75.6	321	6	BD097618	BD097618 Antibody
16	242.6	75.6	814	9	AB064076	AB064076 Homo sapi
17	241	75.1	315	9	HSFAB82VL	Y08148 H.sapiens m
18	240.8	75.0	318	12	AF044455	AF044455 Synthetic
19	240.8	75.0	321	6	AR160977	AR160977 Sequence
20	239.4	74.6	339	9	AB006846	AB006846 Homo sapi
21	237.8	74.1	324	6	AX112586	AX112586 Sequence
22	237.8	74.1	735	6	CQ832185	CQ832185 Sequence
23	237	73.8	324	9	AB095290	AB095290 Homo sapi
24	236.2	73.6	321	6	A29589	A29589 H.sapiens c
25	236.2	73.6	324	12	AF538696	AF538696 Synthetic
26	236.2	73.6	642	9	AB095273	AB095273 Homo sapi
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34	232.8	72.5	917	6	BD248694	BD248694 Immunoglo
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36	231.4	72.1	324	9	AB063929	AB063929 Homo sapi
37	231.4	72.1	333	6	BD097236	BD097236 A therape
38	231.4	72.1	346	9	HSG1B6IGK	X94431 H.sapiens r
39	231.4	72.1	388	9	HSA548508	AJ548508 Homo sapi
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41	231.4	72.1	720	6	CQ840583	CQ840583 Sequence
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ALIGNMENTS

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RESULT 1
A84380
LOCUS       A84380                   321 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 147 from Patent WO9846645.
ACCESSION   A84380
VERSION     A84380.1  GI:6733303
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
            USES THEREOF
  JOURNAL   Patent: WO 9846645-A 147 22-OCT-1998;
            KUFER PETER (DE); RAUM TOBIAS (DE)
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                     RLDIQ"
ORIGIN

  Query Match          100.0%;  Score 321;  DB 6;  Length 321;
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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
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Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
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Db        301 GGGACACGACTGGACATTCAA 321
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RESULT 2
BD075296

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LOCUS       BD075296                321 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel method for the production of anti-human antigen receptors and
            uses thereof.
ACCESSION   BD075296
VERSION     BD075296.1  GI:22620899
KEYWORDS    JP 2001519824-A/25.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Novel method for the production of anti-human antigen receptors and
            uses thereof
  JOURNAL   Patent: JP 2001519824-A 25 23-OCT-2001;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001519824-A/25
            PD   23-OCT-2001
            PF   14-APR-1998 JP 1998543494
            PR   14-APR-1997 EP   97106109.8
            PI   PETER KUFER,TOBIAS RAUM
            PC   C07K16/00,C07K16/30,A61K39/395
            CC   Novel method for the production of anti-human antigen  CC
             receptors and uses
            CC   thereof
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(321).
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 321;  DB 6;  Length 321;
  Best Local Similarity   100.0%;  Pred. No. 2.3e-97;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
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Db        301 GGGACACGACTGGACATTCAA 321
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RESULT 3
BD222938

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LOCUS       BD222938                1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222938
VERSION     BD222938.1  GI:33032708
KEYWORDS    JP 2002521053-A/32.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 32 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/32
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC   (C12N5/00,C12R1:91)
            CC   Heterominibodies
            FH   Key             Location/Qualifiers
            FT   CDS             (39). .(1607).
FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 321;  DB 6;  Length 1630;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-97;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||||||||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 4
BD222939
LOCUS       BD222939                1630 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  Heterominibodies.
ACCESSION   BD222939
VERSION     BD222939.1  GI:33032709
KEYWORDS    JP 2002521053-A/33.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1630)
  AUTHORS   Kufer,P., Dreier,T., Baeuerle,P.A., Borschert,K. and Zettl,F.
  TITLE     Heterominibodies
  JOURNAL   Patent: JP 2002521053-A 33 16-JUL-2002;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            OS   Mus musculus (mouse)
            PN   JP 2002521053-A/33
            PD   16-JUL-2002
            PF   28-JUL-1999 JP 2000562401
            PR   28-JUL-1998 EP   98114082.5
            PI   PETER KUFER,TORSTEN DREIER,PATRICK A BAEUERLE,KATRIN
            BORSCHERT,
            PI   FLORIAN ZETTL
            PC   C12N15/09,A61K35/76,A61K38/00,A61K38/21,A61P35/00,A61P35/02,
            PC   C07K19/00,
            PC   C12N5/10,C12P21/02,G01N33/53,G01N33/53//(C12N5/10,C12R1:91),
            PC   (C12P21/02,C12R1:91),C12N15/00,C12N5/00,A61K37/02,A61K37/66,
            PC   (C12N5/00,C12R1:91)
            CC   Heterominibodies
            FH   Key             Location/Qualifiers
            FT   CDS             (39). .(1610).
FEATURES              Location/Qualifiers
     source           1. .1630
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match           100.0%;  Score 321;  DB 6;  Length 1630;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-97;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||||||||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 5
AX023365
LOCUS       AX023365                1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 36 from Patent WO0006605.
ACCESSION   AX023365
VERSION     AX023365.1  GI:10183777
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 36 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
FEATURES              Location/Qualifiers
     source           1. .1630
                      /organism="Homo sapiens"
                      /mol_type="unassigned DNA"
                      /db_xref="taxon:9606"
     CDS              39. .1610
                      /note="unnamed protein product"
                      /codon_start=1
                      /protein_id="CAC08835.1"
                      /db_xref="GI:10183778"
                      /translation="MGWSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
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                      LSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN
                      TLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTTVTVSSGTPLGDTT
                      HTASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAV
                      LQSSGLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTSGGGGSAP
                      ARSPSPSTQPWEHVNAIQEARRLLNLSRDTAAEMNETVEVISEMFDLQEPTCLQTRLE
                      LYKQGLRGSLTKLKGPLTMMASHYKQHCPPTPETSCATQIITFESFKENLKDFLLVIP
                      FDCWEPVQEHHHHHH"
ORIGIN

  Query Match           100.0%;  Score 321;  DB 6;  Length 1630;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-97;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACACGACTGGACATTCAA 321
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Db        396 GGGACACGACTGGACATTCAA 416


RESULT 6
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AX023367
LOCUS       AX023367                1630 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 38 from Patent WO0006605.
ACCESSION   AX023367
VERSION     AX023367.1  GI:10183779
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P., Zettl,F., Dreier,T., Baeuerle,P.A. and Borschert,K.
  TITLE     Heterominibodies
  JOURNAL   Patent: WO 0006605-A 38 10-FEB-2000;
            KUFER PETER (DE) ; ZETTL FLORIAN (DE) ; DREIER TORSTEN (DE) ;
            BAEUERLE PATRICK A (DE) ; BORSCHERT KATRIN (DE) ; MICROMET GES FUER
            BIOMEDIZINIS (DE)
FEATURES             Location/Qualifiers
     source          1. .1630
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
     CDS             39. .1613
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC08836.1"
                     /db_xref="GI:10183780"
                     /translation="MGWSCIILFLVATATGVHSELQMTQSPSSLSASVGDRVTITCRA
                     SQSISSYLNWYQQKPGQPPKLLIYWASTRESGVPDRFSGSESGTNYTLTISSLQPEDF
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                     LSCAASGFTFSSYGMHWVRQAPGKGLEWVAVISYDGSNKYYADSVKGRFTISRDNSKN
                     TLYLQMNSLRAEDTAVYYCAKDMGWGSGWRPYYYYGMDVWGQGTTVTVSSGTPLGDTT
                     HTRTVAAPSVFIFPPSDEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESV
                     TEQDSKDSTYSLSSTLTLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGECSGGGGSA
                     PTSSSTKKTQLQLEHLLLDLQMILNGINNYKNPKLTRMLTFKFYMPKKATELKHLQCL
                     EEELKPLEEVLNLAQSKNFHLRPRDLISNINVIVLELKGSETTFMCEYADETATIVEF
                     LNRWITFCQSIISTLT"
ORIGIN

  Query Match           100.0%;  Score 321;  DB 6;  Length 1630;
  Best Local Similarity  100.0%;  Pred. No. 2.5e-97;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        336 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 395

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||||||||
Db        396 GGGACACGACTGGACATTCAA 416


RESULT 7
A84374
LOCUS       A84374                  321 bp    DNA     linear   PAT 21-JAN-2000
DEFINITION  Sequence 141 from Patent WO9846645.
ACCESSION   A84374
VERSION     A84374.1  GI:6733297
KEYWORDS    .
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN RECEPTORS AND
            USES THEREOF
  JOURNAL   Patent: WO 9846645-A 141 22-OCT-1998;
            KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES             Location/Qualifiers
     source          1. .321
                     /organism="unidentified"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32644"
     CDS             <1. .>321
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAB69287.1"
                     /db_xref="GI:6733298"
                     /translation="ELQMTQSPSSLSASVGDRVTITCRTSQSISSYLNWYQQKPGQPP
                     KLLIYWASTRESGVPDRFSGSGSGTDFTLTISSLQPEDSATYYCQQSYDIPYTFGQGT
                     KLEIK"
ORIGIN

  Query Match           81.1%;  Score 260.2;  DB 6;  Length 321;
  Best Local Similarity  88.2%;  Pred. No. 1e-76;
  Matches  283;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  |||||||||| ||| ||||||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 8
AX003761
LOCUS       AX003761                321 bp    DNA     linear   PAT 24-AUG-2000
DEFINITION  Sequence 55 from Patent WO9925818.
ACCESSION   AX003761
VERSION     AX003761.1  GI:9927567
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Method of identifying binding site domains that retain the capacity
            of binding to an epitope
  JOURNAL   Patent: WO 9925818-A 55 27-MAY-1999;
            KUFER PETER (DE); RAUM TOBIAS (DE)
FEATURES             Location/Qualifiers
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     source          1. .321
                     /organism="Homo sapiens"
                     /mol_type="unassigned DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             81.1%;  Score 260.2;  DB 6;  Length 321;
  Best Local Similarity   88.2%;  Pred. No. 1e-76;
  Matches  283;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  ||||||||| ||| ||||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 9
BD075293
LOCUS       BD075293                321 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Novel method for the production of anti-human antigen receptors and
            uses thereof.
ACCESSION   BD075293
VERSION     BD075293.1  GI:22620896
KEYWORDS    JP 2001519824-A/22.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P. and Raum,T.
  TITLE     Novel method for the production of anti-human antigen receptors and
            uses thereof
  JOURNAL   Patent: JP 2001519824-A 22 23-OCT-2001;
            MICROMET AG
COMMENT     OS   Homo sapiens (human)
            PN   JP 2001519824-A/22
            PD   23-OCT-2001
            PF   14-APR-1998 JP 1998543494
            PR   14-APR-1997 EP   97106109.8
            PI   PETER KUFER,TOBIAS RAUM
            PC   C07K16/00,C07K16/30,A61K39/395
            CC   Novel method for the production of anti-human antigen  CC
                  receptors and uses
            CC   thereof
            FH   Key             Location/Qualifiers
            FT   CDS             (1). .(321).
FEATURES              Location/Qualifiers
     source           1. .321
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             81.1%;  Score 260.2;  DB 6;  Length 321;
  Best Local Similarity   88.2%;  Pred. No. 1e-76;
  Matches  283;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              |||||||||||||||||||||||||||||||||||||||| ||||| |||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTGCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  ||||||||| ||| ||||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| ||||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 10
BD139668
LOCUS       BD139668                321 bp    DNA     linear   PAT 18-SEP-2002
DEFINITION  A novel method of identifying binding site domains that retain the
            capacity of binding to an epitope.
ACCESSION   BD139668
VERSION     BD139668.1  GI:23234613
KEYWORDS    JP 2002508924-A/53.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kufer,P., Raum,T., Borschert,K., Zettl,F. and Lutterbuese,R.
  TITLE     A novel method of identifying binding site domains that retain the
            capacity of binding to an epitope
  JOURNAL   Patent: JP 2002508924-A 53 26-MAR-2002;
            PETER KUFER
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002508924-A/53
            PD   26-MAR-2002
            PF   16-NOV-1998 JP 2000521184
            PR   17-NOV-1997 EP   97120096.9
            PI   PETER KUFER,TOBIAS RAUM,KATRIN BORSCHERT,FLORIAN ZETTL,RALF
            PI   LUTTERBUESE
            PC   C12N15/09,A61K38/00,A61K38/22,A61K38/43,A61K39/395,C07K14/705,
            PC   C07K16/30,
            PC   C12N1/21,C12N5/10,C12P21/02,C12P21/08,G01N33/566,C12N15/00, PC
              A61K37/02,
            PC   A61K37/24,A61K37/48,C12N5/00
            CC   A novel method of identifying binding site
            domains that retain
            CC             the
            CC   capacity of binding to an epitope
            FH   Key             Location/Qualifiers
            FT   source          1. .321
            FT                   /organism='Homo sapiens (human)'.
FEATURES              Location/Qualifiers
     source           1. .321
                      /organism="Homo sapiens"
                      /mol_type="genomic DNA"
                      /db_xref="taxon:9606"
ORIGIN

  Query Match             81.1%;  Score 260.2;  DB 6;  Length 321;
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  Best Local Similarity   88.2%;  Pred. No. 1e-76;
  Matches  283;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  |||||||| ||| ||||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 11
BD187178
LOCUS       BD187178                324 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Human-typed antibody against blood coagulation factor VIII.
ACCESSION   BD187178
VERSION     BD187178.1  GI:31879467
KEYWORDS    WO 02101040-A/7.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Nakashima,T. and Yuguchi,M.
  TITLE     Human-typed antibody against blood coagulation factor VIII
  JOURNAL   Patent: WO 02101040-A 7 19-DEC-2002;
            JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE,
            TOSHIHIRO NAKASHIMA,MASATO YUGUCHI
COMMENT     OS   Homo sapiens (human)
            PN   WO 02101040-A/7
            PD   19-DEC-2002
            PF   11-JUN-2002 WO 2002JP005783
            PR   12-JUN-2001 JP 01P   177640
            PI   TOSHIHIRO NAKASHIMA,MASATO YUGUCHI
            PC   C12N15/09,C07K16/14,C07K7/06,C07K7/08,C12P21/08,G01N33/53 CC
            Human-typed antibody against blood coagulation factor VIII FH   Key
                     Location/Qualifiers
            FT   source          1. .324
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             76.6%;  Score 245.8;  DB 6;  Length 324;
  Best Local Similarity   85.4%;  Pred. No. 7.9e-72;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||     ||||| |     | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||| | |||||    ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 12
BD187179
LOCUS       BD187179                324 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Human-typed antibody against blood coagulation factor VIII.
ACCESSION   BD187179
VERSION     BD187179.1  GI:31879468
KEYWORDS    WO 02101040-A/8.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 324)
  AUTHORS   Nakashima,T. and Yuguchi,M.
  TITLE     Human-typed antibody against blood coagulation factor VIII
  JOURNAL   Patent: WO 02101040-A 8 19-DEC-2002;
            JURIDICAL FOUNDATION THE CHEMO SERO THERAPEUTIC RESEARCH INSTITUTE,
            TOSHIHIRO NAKASHIMA,MASATO YUGUCHI
COMMENT     OS   Homo sapiens (human)
            PN   WO 02101040-A/8
            PD   19-DEC-2002
            PF   11-JUN-2002 WO 2002JP005783
            PR   12-JUN-2001 JP 01P   177640
            PI   TOSHIHIRO NAKASHIMA,MASATO YUGUCHI
            PC   C12N15/09,C07K16/14,C07K7/06,C07K7/08,C12P21/08,G01N33/53 CC
            Human-typed antibody against blood coagulation factor VIII FH   Key
                     Location/Qualifiers
            FT   source          1. .324
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .324
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

  Query Match             76.6%;  Score 245.8;  DB 6;  Length 324;
  Best Local Similarity   85.4%;  Pred. No. 7.9e-72;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||     ||||| |     | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240
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Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||| |||||||  |||||||||  | |||||   ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 13
AB006842
LOCUS       AB006842                339 bp    mRNA    linear   PRI 09-SEP-1997
DEFINITION  Homo sapiens mRNA for HRV Fab N6-VL, partial cds.
ACCESSION   AB006842
VERSION     AB006842.1  GI:2385484
KEYWORDS    HRV Fab N6-VL.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (sites)
  AUTHORS   Itoh,K. and Suzuki,T.
  TITLE     Human anti-rotavirus Fabs
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 339)
  AUTHORS   Itoh,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (26-AUG-1997) Kunihiko Itoh, Akita University Hospital,
            Pharmaceutical Science; Hondo 1-1-1, Akita, Akita 010, Japan
            (E-mail:itohk@hos.akita-u.ac.jp, Tel:+81-188-34-1111,
            Fax:+81-188-36-2628)
FEATURES             Location/Qualifiers
     source          1. .339
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
                     /tissue_type="PBL"
     CDS             1. .>339
                     /codon_start=1
                     /product="HRV Fab N6-VL"
                     /protein_id="BAA22181.1"
                     /db_xref="GI:2385485"
                     /translation="MAELVMTQSPSSLAASVGDRVTFTCRASQSISSYLNWYQQKPGK
                     APKLLIYAASSLQSGVPSRFSGSGSGTDFTLTISSLQPEDFATYYCQQSYSTPITFGQ
                     GTRLEIKRTVA"
ORIGIN

  Query Match           76.1%;  Score 244.2;  DB 9;  Length 339;
  Best Local Similarity   85.0%;  Pred. No. 2.8e-71;
  Matches  273;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||  ||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db          7 GAGCTCGTGATGACCCAGTCTCCATCCTCCCTGGCTGCATCTGTAGGAGACAGAGTCACC 66

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 TTCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 126

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||    ||||| |     | ||   |||||||
Db        127 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 186

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | |||||  |||||||  |||||||||  |||  |||||||||||||||||  |||||  |||
Db        187 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 246

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||| |||||||  |||||||||  | |||||   ||||||||||||||||||
Db        247 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACTCCGATCACCTTCGGCCAA 306

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        307 GGGACACGACTGGAGATTAAA 327


RESULT 14
BD097614
LOCUS       BD097614                342 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antibody library.
ACCESSION   BD097614
VERSION     BD097614.1  GI:22643188
KEYWORDS    WO 0162907-A/69.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 342)
  AUTHORS   Kurosawa,Y., Akahori,Y., Iba,Y., Morino,K., Shinohara,M.,
            Takahashi,M., Okuno,Y. and Shiraki,K.
  TITLE     Antibody library
  JOURNAL   Patent: WO 0162907-A 69 30-AUG-2001;
            MEDICAL & BIOLOGICAL LABORATORIES CO LTD,YOSHIKAZU KUROSAWA,
            YASUSHI AKAHORI,YOSHITAKA IBA,KAZUHIKO MORINO,MIDORI SHINOHARA,
            MOTOHIDE TAKAHASHI,YOSHINOBU OKUNO,KIMIYASU SHIRAKI
COMMENT     OS   Homo sapiens (human)
            PN   WO 0162907-A/69
            PD   30-AUG-2001
            PF   22-FEB-2001 WO 2001JP001298
            PR   22-FEB-2000 JP 00P    50543
            PI   YOSHIKAZU KUROSAWA,YASUSHI AKAHORI,YOSHITAKA IBA,KAZUHIKO  PI
             MORINO,
            PI   MIDORI SHINOHARA,MOTOHIDE TAKAHASHI,YOSHINOBU OKUNO,KIMIYASU
            PI   SHIRAKI
            PC   C12N15/09,C07K16/00//C12P21/08
            CC   Antibody library
            FH   Key             Location/Qualifiers
            FT   source          1. .342
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .342
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                     /db_xref="taxon:9606"
ORIGIN

  Query Match           76.1%;  Score 244.2;  DB 6;  Length 342;
  Best Local Similarity   85.0%;  Pred. No. 2.8e-71;
  Matches  273;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||    ||||| |     | ||   |||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | |||||  |||||||  |||||||||  |||  |||||||||||||||||  |||||  |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
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RESULT 15
BD097618
LOCUS       BD097618                321 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  Antibody library.
ACCESSION   BD097618
VERSION     BD097618.1  GI:22643192
KEYWORDS    WO 0162907-A/73.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 321)
  AUTHORS   Kurosawa,Y., Akahori,Y., Iba,Y., Morino,K., Shinohara,M.,
            Takahashi,M., Okuno,Y. and Shiraki,K.
  TITLE     Antibody library
  JOURNAL   Patent: WO 0162907-A 73 30-AUG-2001;
            MEDICAL & BIOLOGICAL LABORATORIES CO LTD,YOSHIKAZU KUROSAWA,
            YASUSHI AKAHORI,YOSHITAKA IBA,KAZUHIKO MORINO,MIDORI SHINOHARA,
            MOTOHIDE TAKAHASHI,YOSHINOBU OKUNO,KIMIYASU SHIRAKI
COMMENT     OS   Homo sapiens (human)
            PN   WO 0162907-A/73
            PD   30-AUG-2001
            PF   22-FEB-2001 WO 2001JP001298
            PR   22-FEB-2000 JP 00P    50543
            PI   YOSHIKAZU KUROSAWA,YASUSHI AKAHORI,YOSHITAKA IBA,KAZUHIKO  PI
             MORINO,
            PI   MIDORI SHINOHARA,MOTOHIDE TAKAHASHI,YOSHINOBU OKUNO,KIMIYASU
            PI   SHIRAKI
            PC   C12N15/09,C07K16/00//C12P21/08
            CC   Antibody library
            FH   Key             Location/Qualifiers
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            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           75.6%;  Score 242.6;  DB 6;  Length 321;
  Best Local Similarity  84.7%;  Pred. No. 9.7e-71;
  Matches  272;  Conservative    0;  Mismatches   49;  Indels    0;  Gaps    0;

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Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||  || || ||    ||||| |    | ||   ||||||||
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Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||  | |||||   || ||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
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Search completed: December  7, 2004, 08:53:05
Job time : 1816.78 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 6, 2004, 22:52:33 ; Search time 271.757 Seconds
(without alignments)
6200.629 Million cell updates/sec

Title: US-09-403-107-147
Perfect score: 321
Sequence: 1 gagctccagatgacccagtc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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10: geneseqn2003cs:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	2	AAV68539	Aav68539 Nucleotid
2	321	100.0	1630	3	AAZ50588	Aaz50588 HD70scFv-
3	321	100.0	1630	3	AAZ50587	Aaz50587 HD70scFv-
4	260.2	81.1	321	2	AAV68536	Aav68536 Nucleotid
5	260.2	81.1	321	2	AAX77237	Aax77237 Human kap
6	249	77.6	321	11	ADO51603	Ado51603 Human TAG
7	245.8	76.6	324	10	AAL52122	Aal52122 Human ant
8	244.2	76.1	342	4	AAH47727	Aah47727 Nucleotid
9	242.6	75.6	321	4	AAH47731	Aah47731 Nucleotid
10	240.8	75.0	321	5	AAH68651	Aah68651 Human ant
11	240.8	75.0	321	9	ACD45315	Acd45315 Anti-Rh(D
12	240.2	74.8	321	12	ADO36505	Ado36505 Human ant
13	240.2	74.8	321	12	ADO36497	Ado36497 Human ant
14	238.6	74.3	327	10	ADD89879	Add89879 Human ant
15	237.8	74.1	321	12	ADP22249	Adp22249 Human ant
16	237.8	74.1	324	4	AAS03434	Aas03434 DNA encod
17	236.2	73.6	321	11	ADO51602	Ado51602 Human TAG
18	236.2	73.6	321	12	ADP22235	Adp22235 Human ant
19	236.2	73.6	321	12	ADP22253	Adp22253 Human ant
20	236.2	73.6	458	12	ADK52349	Adk52349 Human ant
21	235	73.2	1106	6	ABQ54241	Abq54241 Human ova
22	234.4	73.0	936	3	AAA27390	Aaa27390 Human IGF
23	233	72.6	321	12	ADP22243	Adp22243 Human ant
24	232.8	72.5	917	3	AAA27381	Aaa27381 Human IGF
25	231.4	72.1	333	5	AAH74684	Aah74684 Nucleotid
26	231.4	72.1	333	10	ABT34320	Abt34320 Hepatitis
27	231.4	72.1	720	2	AAX36070	Aax36070 DNA encod
28	231.4	72.1	720	10	ABZ76706	Abz76706 Human ser
29	231.4	72.1	720	12	ADL92368	Adl92368 Human pha
30	231.4	72.1	900	5	AAH74688	Aah74688 Nucleotid
31	231.4	72.1	900	10	ABT34324	Abt34324 Hepatitis
32	229.8	71.6	321	9	AAD57375	Aad57375 Human 5F1
33	229.8	71.6	324	10	AAL52120	Aal52120 Human ant
34	229.8	71.6	396	2	AAT75423	Aat75423 Human ant
35	229.8	71.6	684	4	AAH30052	Aah30052 TRO005 ka
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39	228.2	71.1	321	11	ADO51601	Ado51601 Human TAG
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41	228.2	71.1	324	4	AAF29073	Aaf29073 Human HIV
42	228.2	71.1	324	12	ADL92385	Adl92385 Anti-HSA
43	228.2	71.1	714	3	AAA46899	Aaa46899 DNA encod
44	228.2	71.1	714	10	AAD54350	Aad54350 Human 11.
45	228.2	71.1	819	10	AAD59178	Aad59178 Human Ig

ALIGNMENTS

RESULT 1
AAV68539
ID AAV68539 standard; DNA; 321 BP.
XX
AC AAV68539;
XX
DT 16-FEB-1999 (first entry)
XX
DE Nucleotide sequence of human kappa 5.1 light chain variable region.
XX
KW Human; kappa 5.1 light chain variable region; receptor; antigen; tumour;
KW auto-immune disease; graft rejection; allergy; inflammatory disease;
KW endocrine disease; degenerative disease; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .321
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XX
PN WO9846645-A2.
XX
PD 22-OCT-1998.
XX
PF 14-APR-1998; 98WO-EP002180.
XX
PR 14-APR-1997; 97EP-00106109.
XX
PA (KUFE/) KUFER P.
PA (RAUM/) RAUM T.
XX
PI Kufer P, Raum T;
XX
DR WPI; 1998-594564/50.
DR P-PSDB; AAW68539.
XX
PT Production of anti-human antigen receptors - by selecting a combination
PT of functionally rearranged VH and VL immunoglobulin chains expressed from
PT a recombinant vector.
XX
PS Claim 9; Fig 9; 84pp; English.
XX
CC This is the nucleotide sequence of the human kappa light chain variable

CC region, used in the method of the invention. for providing receptors that
CC can be used for targeting antigens in humans without being immunogenic
CC themselves. Such receptors can be used for treating diseases such as
CC tumours or auto-immune diseases, graft rejection after transplantation,
CC infectious diseases by targeting cellular receptors as well as allergic,
CC inflammatory, endocrine and degenerative diseases by targeting key
CC molecules involved in the pathological process
XX
SQ Sequence 321 BP; 81 A; 93 C; 72 G; 75 T; 0 U; 0 Other;

Query Match 100.0%; Score 321; DB 2; Length 321;
Best Local Similarity 100.0%; Pred. No. 1.3e-93;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
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Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy        301 GGGACACGACTGGACATTCAA 321
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Db        301 GGGACACGACTGGACATTCAA 321
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RESULT 2
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ID AAZ50588 standard; DNA; 1630 BP.
XX
AC AAZ50588;
XX
DT 23-MAY-2000 (first entry)
XX
DE HD70scFv-Ck-interleukin 2 encoding DNA.
XX
KW HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW epithelial cell adhesion molecule; inflammatory cytokine; IL-2;
KW interleukin-2; Ck-domain; kappa light chain constant domain;
KW heterominibody; multifunctional compound; immunoglobulin; cytostatic;
KW immunostimulatory; antileukaemia; diagnosis; prevention;
KW antiproliferative; treatment; malignant; haematopoietic cell; lymphoma;
KW leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
XX
OS Homo sapiens.
XX
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XX
PN WO200006605-A2.
XX
PD 10-FEB-2000.
XX
PF 28-JUL-1999; 99WO-EP005416.
XX
PR 28-JUL-1998; 98EP-00114082.
XX
PA (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI Kufer P, Dreier T, Baeuerle PA, Borschert K, Zettl F;
XX
DR WPI; 2000-195265/17.
DR P-PSDB; AAY44995.
XX
PT New multifunctional compounds useful for preventing and/or treating
PT malignant cell growth and for detection and diagnosis.
XX
PS Claim 8; Fig 55B; 166pp; English.
XX
CC The patent discloses heterominibodies which are multifunctional compounds
CC produceable in a mammalian host cell as a secretable and fully functional
CC heterodimer of two polypeptide chains, where one of the polypeptide
CC chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC heavy chain) and the other chain comprises CL-domain (constant domain of
CC an immunoglobulin light chain). The polypeptide chains further comprise,
CC fused to the constant domains at least two (poly)peptides having
CC different receptor or ligand functions, where further at least two of the
CC different (poly)peptides lack an intrinsic affinity for one another and
CC are linked via the constant domains. The heterominibodies have
CC cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC activities. These compounds can be used for diagnosing, preventing and
CC treating malignant cell growth related to malignancies of haematopoietic
CC cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC melanomas and sarcomas. The present sequence is a DNA encoding right
CC chain of a heterominibody comprising HD70 single-chain Fv (scFv) fragment
CC N-terminally linked to human Ck domain (constant domain of immunoglobulin
CC -kappa light chain) which bears at its C-terminus the human inflammatory
CC cytokine interleukin-2 (IL-2). HD70 scFv specifically recognises the
CC human epithelial cell adhesion molecule (EpCAM) also called 17-1A antigen
XX
SQ Sequence 1630 BP; 445 A; 410 C; 408 G; 367 T; 0 U; 0 Other;

Query Match 100.0%; Score 321; DB 3; Length 1630;
Best Local Similarity 100.0%; Pred. No. 2.5e-93;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
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Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        276 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 335

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
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Qy        301 GGGACACGACTGGACATTCAA 321
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Db        396 GGGACACGACTGGACATTCAA 416
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RESULT 3
AAZ50587
ID AAZ50587 standard; DNA; 1630 BP.
XX
AC AAZ50587;
XX
DT 23-MAY-2000 (first entry)

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DE   HD70scFv-CH1-GM-CSF chain encoding DNA.
XX
KW   HD70; single-chain variable fragment; scFv; 17-1A antigen; human; EpCAM;
KW   epithelial cell adhesion molecule; inflammatory cytokine; GM-CSF;
KW   granulocyte/macrophage colony stimulating factor; heterominibody;
KW   CH1-domain; multifunctional compound; heavy chain constant domain;
KW   immunoglobulin; cytostatic; immunostimulatory; antileukaemia; diagnosis;
KW   antiproliferative; prevention; treatment; malignant; haematopoietic cell;
KW   lymphoma; leukaemia; solid tumour; carcinoma; melanoma; sarcoma; ds.
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OS   Homo sapiens.
XX
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PN   WO200006605-A2.
XX
PD   10-FEB-2000.
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PF   28-JUL-1999;   99WO-EP005416.
XX
PR   28-JUL-1998;   98EP-00114082.
XX
PA   (MICR-) MICROMET GES BIOMEDIZINISCHE FORSCHUNG.
XX
PI   Kufer P,  Dreier T,  Baeuerle PA,  Borschert K,  Zettl F;
XX
DR   WPI; 2000-195265/17.
DR   P-PSDB; AAY44994.
XX
PT   New multifunctional compounds useful for preventing and/or treating
PT   malignant cell growth and for detection and diagnosis.
XX
PS   Claim 8; Fig 55A; 166pp; English.
XX
CC   The patent discloses heterominibodies which are multifunctional compounds
CC   produceable in a mammalian host cell as a secretable and fully functional
CC   heterodimer of two polypeptide chains, where one of the polypeptide
CC   chains comprises, a CH1-domain (constant domain of an immunoglobulin
CC   heavy chain) and the other chain comprises CL-domain (constant domain of
CC   an immunoglobulin light chain). The polypeptide chains further comprise,
CC   fused to the constant domains at least two (poly)peptides having
CC   different receptor or ligand functions, where further at least two of the
CC   different (poly)peptides lack an intrinsic affinity for one another and
CC   are linked via the constant domains. The heterominibodies have
CC   cytostatic, immunostimulatory, antileukaemia and antiproliferative
CC   activities. These compounds can be used for diagnosing, preventing and
CC   treating malignant cell growth related to malignancies of haematopoietic
CC   cells e.g. lymphomas and leukaemias, or to solid tumours e.g. carcinomas,
CC   melanomas and sarcomas. The present sequence is a DNA encoding left chain
CC   of a heterominibody comprising HD70 single-chain Fv (scFv) fragment N-
CC   terminally linked to human CH1 domain which bears at its C-terminus the
CC   human inflammatory cytokine granulocyte/macrophage colony stimulating
CC   factor (GM-CSF), plus a hexahistidine sequence for ease of purification.
CC   HD70 scFv specifically recognises the human epithelial cell adhesion
CC   molecule (EpCAM) also called 17-1A antigen
XX
SQ   Sequence 1630 BP; 376 A; 484 C; 437 G; 333 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 321;  DB 3;  Length 1630;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-93;
  Matches  321;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db         96 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 155

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
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Db        156 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 215

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        216 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 275

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
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Qy        301 GGGACACGACTGGACATTCAA 321
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Db        396 GGGACACGACTGGACATTCAA 416


RESULT 4
AAV68536
ID   AAV68536 standard; DNA; 321 BP.
XX
AC   AAV68536;
XX
DT   16-FEB-1999  (first entry)
XX
DE   Nucleotide sequence of human Kappa 8 light chain variable region.
XX
KW   Human; kappa 8 light chain variable region; receptor; antigen; tumour;
KW   auto-immune disease; graft rejection; allergy; inflammatory disease;
KW   endocrine disease; degenerative disease; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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XX
PN   WO9846645-A2.
XX
PD   22-OCT-1998.
XX
PF   14-APR-1998;   98WO-EP002180.
XX
PR   14-APR-1997;   97EP-00106109.
XX
PA   (KUFE/) KUFER P.
PA   (RAUM/) RAUM T.
XX
PI   Kufer P,  Raum T;
XX
DR   WPI; 1998-594564/50.
DR   P-PSDB; AAW80814.
XX
PT   Production of anti-human antigen receptors - by selecting a combination
PT   of functionally rearranged VH and VL immunoglobulin chains expressed from
PT   a recombinant vector.
XX
PS   Claim 9; Fig 6; 84pp; English.
XX
CC   This is the nucleotide sequence of the human kappa 8 light chain variable
CC   region, used in the method of the invention. for providing receptors that
CC   can be used for targeting antigens in humans without being immunogenic
CC   themselves. Such receptors can be used for treating diseases such as
CC   tumours or auto-immune diseases, graft rejection after transplantation,
CC   infectious diseases by targeting cellular receptors as well as allergic,
CC   inflammatory, endocrine and degenerative diseases by targeting key
CC   molecules involved in the pathological process
XX
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```
SQ   Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;

  Query Match             81.1%;  Score 260.2;  DB 2;  Length 321;
  Best Local Similarity   88.2%;  Pred. No. 6.6e-74;
  Matches  283;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  ||||||||| ||| |||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 5
AAX77237
ID   AAX77237 standard; DNA; 321 BP.
XX
AC   AAX77237;
XX
DT   04-AUG-1999  (first entry)
XX
DE   Human kappa 8 light chain variable region encoding DNA.
XX
KW   Binding site domain; BSD; epitope; fusion protein; therapeutic; cancer;
KW   autoimmune disease; scFv-antibody; single-chain Fv; ss.
XX
OS   Homo sapiens.
XX
PN   WO9925818-A1.
XX
PD   27-MAY-1999.
XX
PF   16-NOV-1998;   98WO-EP007313.
XX
PR   17-NOV-1997;   97EP-00120096.
XX
PA   (KUFE/) KUFER P.
XX
PI   Kufer P,  Raum T,  Borschert K,  Zettl F,  Lutterbuese R;
XX
DR   WPI; 1999-338004/28.
DR   P-PSDB; AAY17955.
XX
PT   Phage display system for identification of binding site domains retaining
PT   capacity to bind an epitope.
XX
PS   Disclosure; Fig 3.2; 152pp; English.
XX
CC   The invention relates to a method of identifying binding site domains
CC   (BSD) that retain the capacity of binding to a predetermined epitope when
CC   positioned C-terminal of at least one further domain in a recombinant bi-
CC   or multivalent polypeptide. The method comprises (a) testing a panel of
CC   BSD displayed on the surface of a biological display system as part of a
CC   fusion protein for binding to a predetermined epitope, where the fusion
CC   protein comprises an additional domain positioned N-terminal of the BSD
CC   and an amino acid sequence that mediates anchoring of the fusion protein
CC   to the surface of the display system; and (b) identifying a BSD that
CC   binds to the predetermined epitope. The method is useful to identify bi-
CC   or multivalent polypeptides that comprise antibody binding sites capable
CC   of efficiently binding to the corresponding antigen. The polypeptides or
CC   antibodies identified by the method are useful therapeutically and
CC   diagnostically, for e.g. cancer and autoimmune diseases. ScFv-antibody
CC   fragments that bind independently of their position within bifunctional
CC   single-chain fusion proteins can be isolated from combinatorial antibody
CC   libraries using the new in vitro method
XX
SQ   Sequence 321 BP; 81 A; 91 C; 75 G; 74 T; 0 U; 0 Other;

  Query Match             81.1%;  Score 260.2;  DB 2;  Length 321;
  Best Local Similarity   88.2%;  Pred. No. 6.6e-74;
  Matches  283;  Conservative    0;  Mismatches   38;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  ||||||||| ||| |||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 6
ADO51603
ID   ADO51603 standard; DNA; 321 BP.
XX
AC   ADO51603;
XX
DT   15-JUL-2004  (first entry)
XX
DE   Human TAG-72 antibody-related KCS18 gene SeqID13.
XX
KW   semi-human monoclonal antibody; tumour-associated glycoprotein antigen;
KW   TAG-72; human light chain; cancer; AKA; HzK; VK1;
KW   human immunoglobulin kappa light chain germline; gene; ds; human.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .321
FT                   /*tag=  a
FT                   /product= "Human TAG-72 antibody-related KCS18 protein"
FT                   /partial
FT                   /note= "No start or stop codon"
XX
PN   KR2003013633-A.
XX
PD   15-FEB-2003.
XX
PF   08-AUG-2001; 2001KR-00047737.
XX
PR   08-AUG-2001; 2001KR-00047737.
XX
```

```
PA   (KORE-) KOREA RES INST BIOSCIENCE & BIOTECHNOLOG.
XX
PI   Hong HJ,  Kim SJ;
XX
DR   WPI; 2003-500992/47.
DR   P-PSDB; ADO51598.
XX
PT   Semi-human monoclonal antibody binding to tumor-associated glycoprotein
PT   antigen tag-72 and human light chain comprising the same, useful for
PT   diagnosing and treating cancer.
XX
PS   Claim 13; SEQ ID NO 18; 1pp; Korean.
XX
CC   This invention relates to a novel semi-human monoclonal antibody binding
CC   to tumour-associated glycoprotein antigen TAG-72 and a human light chain
CC   comprising the same. The semi-human monoclonal antibody has a human light
CC   chain of which amino acid sequence is completely derived from the human,
CC   therefore it is useful for the diagnosis and treatment of cancer. The
CC   semi-human monoclonal antibody specifically binds to TAG-72 antigen of
CC   which the light chain of human antibody AKA/HzK is substituted with the
CC   light chain of a human derived antibody. The light chain of the human
CC   derived antibody is preferably composed of amino acid sequence derived
CC   from the VK1 family of the human immunoglobulin kappa light chain
CC   germline. The present sequence is that of a gene which encodes a human
CC   KCS protein which is related to the novel semi-human TAG-72 antibody of
CC   the invention.
XX
SQ   Sequence 321 BP; 87 A; 86 C; 73 G; 75 T; 0 U; 0 Other;

  Query Match             77.6%;  Score 249;  DB 11;  Length 321;
  Best Local Similarity   86.0%;  Pred. No. 2.8e-70;
  Matches  276;  Conservative    0;  Mismatches   45;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAATCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGGGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||||||  || || ||   ||||||||      |||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATAAGGCATCTAGTTTAGAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | ||||||||||||| |||||||||| | | ||||||||||||||||||||||||||||
Db        181 AGGTTCAGCGGCAGTGGATCTGGGACAGAATTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              || ||||||| |||||| |  |||||||| || ||| |   || ||||||||||||||||
Db        241 GATGATTTTGGTACTTATTACTGTCAACAGACTTACATTGCCCCCATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 7
AAL52122
ID   AAL52122 standard; DNA; 324 BP.
XX
AC   AAL52122;
XX
DT   29-MAY-2003  (first entry)
XX
DE   Human anti-blood coagulation factor VIII antibody-related gene #4.
XX
KW   Human; gene; ds; anti-blood coagulation factor VIII antibody;
KW   FVIII antibody; anti-thrombotic; thrombosis; activated FVIII.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .324
FT                   /*tag=  a
FT                   /partial
FT                   /product= "Human VIII antibody-related protein #4"
FT                   /note= "No start or stop codon is given"
XX
PN   WO2002101040-A1.
XX
PD   19-DEC-2002.
XX
PF   11-JUN-2002; 2002WO-JP005783.
XX
PR   12-JUN-2001; 2001JP-00177640.
XX
PA   (KAGA ) CHEMO-SERO-THERAPEUTIC RES INST.
XX
PI   Nakashima T,  Yuguchi M;
XX
DR   WPI; 2003-148804/14.
DR   P-PSDB; AAO16706.
XX
PT   Human-type anti-blood coagulation factor VIII antibody, applicable in
PT   antithrombotics for prevention or treatment of thrombosis, in diagnosis
PT   of activated FVIII, and for maintaining low coagulation state.
XX
PS   Disclosure; Page 28; 39pp; Japanese.
XX
CC   The invention comprises the amino acid and coding sequence of a human
CC   anti-blood coagulation factor VIII (FVIII) antibody, which has an
CC   inhibitory activity on the coagulation activity of human FVIII. The
CC   antibody is applicable in anti-thrombotics for prevention or treatment of
CC   thrombosis, and in the diagnosis of activated FVIII. The present DNA
CC   sequence encodes a human FVIII antibody-related protein
XX
SQ   Sequence 324 BP; 87 A; 88 C; 73 G; 76 T; 0 U; 0 Other;

  Query Match             76.6%;  Score 245.8;  DB 10;  Length 324;
  Best Local Similarity   85.4%;  Pred. No. 3.1e-69;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||||||  || || ||    |||||  |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | |||||  ||||||| |||||||||| ||| ||||||||||||||||||  ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||| |||||||  |||||||||  | |||||   ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 8
AAH47727
ID   AAH47727 standard; DNA; 342 BP.
XX
AC   AAH47727;
XX
DT   30-NOV-2001  (first entry)
```

XX
DE Nucleotide sequence of seq Id No. 70.
XX
KW Gene library; immunoglobulin; antibody library; human; ds.
XX
OS Homo sapiens.
XX
PN WO200162907-A1.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-JP001298.
XX
PR 22-FEB-2000; 2000JP-00050543.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
DR WPI; 2001-565420/63.
DR P-PSDB; AAG65563.
XX
PT Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
PS Examples; p 146-147; 181pp; Japanese.
XX
CC The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
SQ Sequence 342 BP; 91 A; 93 C; 78 G; 80 T; 0 U; 0 Other;

Query Match 76.1%; Score 244.2; DB 4; Length 342;
Best Local Similarity 85.0%; Pred. No. 1e-68;
Matches 273; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||    ||||| |    | ||   |||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | ||||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||   |||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321
```

RESULT 9
AAH47731
ID AAH47731 standard; DNA; 321 BP.
XX
AC AAH47731;
XX
DT 30-NOV-2001 (first entry)
XX
DE Nucleotide sequence of seq Id No. 74.
XX
KW Gene library; immunoglobulin; antibody library; human; ds.
XX
OS Homo sapiens.
XX
PN WO200162907-A1.
XX
PD 30-AUG-2001.
XX
PF 22-FEB-2001; 2001WO-JP001298.
XX
PR 22-FEB-2000; 2000JP-00050543.
XX
PA (MEDI-) MEDICAL & BIOLOGICAL LAB CO LTD.
XX
PI Kurosawa Y, Akahori Y, Iba Y, Morino K, Shinohara M, Takahashi M;
PI Okuno Y, Shiraki K;
XX
DR WPI; 2001-565420/63.
DR P-PSDB; AAG65567.
XX
PT Producing gene libraries and antibody libraries, involves selecting a
PT light chain that binds to a heavy chain product to produce a functional
PT formation, and producing a gene library of the light chain variable
PT regions.
XX
PS Examples; p 149; 181pp; Japanese.
XX
CC The invention relates to producing gene libraries, comprising
CC immunoglobulin light and heavy variable region. The method involves
CC selecting light chain that binds with the heavy chain product to produce
CC a functional conformation, producing a gene library comprising a
CC collection of these light chain variable genes, and combining with gene
CC library of heavy chain variable genes. The method is used for production
CC of gene and antibody libraries
XX
SQ Sequence 321 BP; 87 A; 87 C; 72 G; 75 T; 0 U; 0 Other;

Query Match 75.6%; Score 242.6; DB 4; Length 321;
Best Local Similarity 84.7%; Pred. No. 3.4e-68;
Matches 272; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCGTGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||    ||||| |    | ||   |||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | ||||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||   |||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321
```

RESULT 10

```
AAH68651
ID   AAH68651 standard; DNA; 321 BP.
XX
AC   AAH68651;
XX
DT   14-SEP-2001  (first entry)
XX
DE   Human anti-Rh(D) chain I06 nucleotide sequence.
XX
KW   Human; anti-Rh(D) antibody; Rh(D) binding protein; immunostimulant;
KW   red blood cell; Rh phenotype; diagnosis; therapeutic; ds.
XX
OS   Homo sapiens.
XX
PN   US6255455-B1.
XX
PD   03-JUL-2001.
XX
PF   29-JAN-1999;   99US-00240274.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2001-388931/41.
DR   P-PSDB; AAG93594.
XX
PT   New isolated protein, preferably a human anti-Rh(D) antibody for use in
PT   diagnostics requiring a human instead of an animal antibody and in
PT   therapeutic medicine.
XX
PS   Example 2; Col 55; 162pp; English.
XX
CC   The present invention describes an isolated Rh(D) binding protein,
CC   preferably a human antibody, (I) having an amino acid sequence comprising
CC   one of the sequences (S) given in AAG93558 to AAG93669. (I) has
CC   immunostimulant activity, and can be used as an immune system stimulant.
CC   (I) can be used in diagnostic and therapeutic medicine. The antibodies
CC   are used in diagnostics that require human antibodies instead of animal
CC   antibodies, such as determine the Rh phenotype of human red blood cells.
CC   AAH68615 to AAH68726 represent the nucleotide sequence which encode
CC   AAG93558 to AAG93669. AAG93670 to AAG93697 represent anti-Rh(D) heavy
CC   chain CDR3 amino acid sequences which are given in the exemplification of
CC   the present invention
XX
SQ   Sequence 321 BP; 86 A; 90 C; 73 G; 72 T; 0 U; 0 Other;

  Query Match             75.0%;  Score 240.8;  DB 5;  Length 321;
  Best Local Similarity   85.1%;  Pred. No. 1.3e-67;
  Matches  269;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||||  | |||||   ||||||||||||||||||||||

Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
              ||||||||| ||| ||
Db        303 ACGACTGGAGATTAAA 318


RESULT 11
ACD45315
ID   ACD45315 standard; DNA; 321 BP.
XX
AC   ACD45315;
XX
DT   12-SEP-2003  (first entry)
XX
DE   Anti-Rh(D) chain I06 DNA.
XX
KW   Human; ds; gene; RH(D) binding protein; blood typing; blood product;
KW   magnetically activated cell sorting.
XX
OS   Homo sapiens.
XX
PN   US2003040605-A1.
XX
PD   27-FEB-2003.
XX
PF   04-MAY-2001; 2001US-00848798.
XX
PR   11-OCT-1996;   96US-0028550P.
PR   27-JUN-1997;   97US-00884045.
PR   10-APR-1998;   98US-0081380P.
PR   29-JAN-1999;   99US-00240274.
XX
PA   (UYPE-) UNIV PENNSYLVANIA.
XX
PI   Siegel DL;
XX
DR   WPI; 2003-512273/48.
DR   P-PSDB; ABO27401.
XX
PT   New human Rh(D)-binding protein useful for various diagnostic and
PT   therapeutic applications, including typing of blood or blood products.
XX
PS   Claim 12; Page 40; 187pp; English.
XX
CC   The invention relates to an isolated Rh(D) binding protein. The protein
CC   can be used for magnetically activated cell sorting. The protein is
CC   useful in various diagnostic and therapeutic applications in humans,
CC   including typing of blood or blood products. The present sequence
CC   represents DNA encoding a human anti-Rh(D) chain
XX
SQ   Sequence 321 BP; 86 A; 90 C; 73 G; 72 T; 0 U; 0 Other;

  Query Match             75.0%;  Score 240.8;  DB 9;  Length 321;
  Best Local Similarity   85.1%;  Pred. No. 1.3e-67;
  Matches  269;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242
```

```
Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||||  | |||||   |||||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
              ||||||||| ||| ||
Db        303 ACGACTGGAGATTAAA 318
```

RESULT 12
ADO36505
ID ADO36505 standard; cDNA; 321 BP.
XX
AC ADO36505;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human anti-heparanase IE7 Vk encoding cDNA SEQ ID NO:19.
XX
KW human; monoclonal antibody; heparanase; heparanase inhibitor;
KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
KW neuroprotective; nootropic; heparanase antagonist; cancer; tumour;
KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
KW autoimmune disease; arthritis; asthma; lupus erythematosus;
KW allograft rejection; vascular restenosis; atherosclerosis;
KW Alzheimer's disease; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .321
FT   /*tag= a
FT   /product= "anti-heparanase IE7 Vk"
XX
PN WO2004043989-A2.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US035464.
XX
PR 07-NOV-2002; 2002US-0424803P.
XX
PA (MEDA-) MEDAREX INC.
PA (CELL-) CELLTECH R & D.
XX
PI Huang H, Holmes S, Mason S;
XX
DR WPI; 2004-411694/38.
DR P-PSDB; ADO36506.
XX
PT New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX
PS Claim 8; SEQ ID NO 19; 108pp; English.
XX
CC The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and nootropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence encodes a human anti-
CC heparanase IE7 Vk amino acid sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 321 BP; 81 A; 87 C; 76 G; 77 T; 0 U; 0 Other;

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  Query Match             74.8%;  Score 240.2;  DB 12;  Length 321;
  Best Local Similarity   84.9%;  Pred. No. 2e-67;
  Matches  269;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          5 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 TCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64

Qy         65 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGAC 124
              |||||||||||||||| ||||||||||   ||||   ||||||||||||||||||||
Db         65 CTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGA 124

Qy        125 AGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGAT 184
              |  |||||||||| || || ||    || || |    ||||   ||||||||     | |
Db        125 AAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT 184

Qy        185 TCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244
              |||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||||||
Db        185 TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244

Qy        245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGA 304
              ||||||| ||||| |  |||||||||| | | ||||  ||||||||||||||||||||||
Db        245 ATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCGATCACCTTCGGCCAAGGGA 304

Qy        305 CACGACTGGACATTCAA 321
              |||||||||| ||| ||
Db        305 CACGACTGGAGATTAAA 321
```

RESULT 13
ADO36497
ID ADO36497 standard; cDNA; 321 BP.
XX
AC ADO36497;
XX
DT 12-AUG-2004 (first entry)
XX
DE Human anti-heparanase 13B2 VL encoding cDNA SEQ ID NO:11.
XX
KW human; monoclonal antibody; heparanase; heparanase inhibitor;
KW anti-heparanase antibody; cytostatic; immunosuppressive; antiarthritic;
KW antiasthmatic; antiinflammatory; dermatological; antiarteriosclerotic;
KW neuroprotective; nootropic; heparanase antagonist; cancer; tumour;
KW melanoma; lymphoma; prostate carcinoma; pancreatic carcinoma;
KW bladder carcinoma; fibrosarcoma; rhabdomyosarcoma; mastocytoma;
KW mammary adenocarcinoma; leukaemia; rheumatoid fibroblast;
KW autoimmune disease; arthritis; asthma; lupus erythematosus;
KW allograft rejection; vascular restenosis; atherosclerosis;
KW Alzheimer's disease; gene; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   1. .321
FT   /*tag= a
FT   /product= "anti-heparanase 13B2 VL"
XX
PN WO2004043989-A2.
XX
PD 27-MAY-2004.
XX
PF 05-NOV-2003; 2003WO-US035464.
XX
PR 07-NOV-2002; 2002US-0424803P.
XX
PA (MEDA-) MEDAREX INC.
PA (CELL-) CELLTECH R & D.
XX

PI Huang H, Holmes S, Mason S;
XX
DR WPI; 2004-411694/38.
DR P-PSDB; ADO36498.
XX
PT New human monoclonal antibody to heparanase, for use in treating or
PT preventing cancer, autoimmune disease, arthritis, asthma, lupus
PT erythematosus, allograft rejection, atherosclerosis, and Alzheimer's
PT disease.
XX
PS Claim 8; SEQ ID NO 11; 108pp; English.
XX
CC The present invention describes an isolated human monoclonal antibody
CC which binds to and inhibits activity of human heparanase. Human anti-
CC heparanase antibodies of the present invention have cytostatic,
CC immunosuppressive, antiarthritic, antiasthmatic, antiinflammatory,
CC dermatological, antiarteriosclerotic, neuroprotective and nootropic
CC activities, and can be used as heparanase antagonists. The antibody,
CC methods and compositions of the present invention are useful in treating
CC or preventing cancer or tumours, e.g. melanoma, lymphoma, prostate
CC carcinoma, pancreatic carcinoma, bladder carcinoma, fibrosarcoma,
CC rhabdomyosarcoma, mastocytoma, mammary adenocarcinoma, leukaemia or a
CC rheumatoid fibroblast, autoimmune disease, arthritis, asthma, lupus
CC erythematosus, allograft rejection, vascular restenosis, atherosclerosis,
CC and Alzheimer's disease. The present sequence encodes a human anti-
CC heparanase 13B2 VL amino acid sequence, which is used in the
CC exemplification of the present invention.
XX
SQ Sequence 321 BP; 81 A; 87 C; 76 G; 77 T; 0 U; 0 Other;

Query Match 74.8%; Score 240.2; DB 12; Length 321;
Best Local Similarity 84.9%; Pred. No. 2e-67;
Matches 269; Conservative 0; Mismatches 48; Indels 0; Gaps 0;

```
Qy          5 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 TCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64

Qy         65 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGAC 124
              |||||||||||||||| |||||||||    ||||   ||||||||||||||||||||
Db         65 CTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGA 124

Qy        125 AGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGAT 184
              | |||||||||| || || ||    || || |    ||||   ||||||||     | |
Db        125 AAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT 184

Qy        185 TCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244
              |||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||||
Db        185 TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244

Qy        245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGA 304
              ||||||| ||||| |  |||||||||| | | ||||  ||||||||||||||||||||||
Db        245 ATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCGATCACCTTCGGCCAAGGGA 304

Qy        305 CACGACTGGACATTCAA 321
              ||||||||| ||| ||
Db        305 CACGACTGGAGATTAAA 321
```

RESULT 14
ADD89879
ID ADD89879 standard; cDNA; 327 BP.
XX
AC ADD89879;
XX
DT 29-JAN-2004 (first entry)
XX
DE Human anti-TNF antibody 9C1A light chain variable region coding sequence.
XX
KW Human; Tumour necrosis factor; TNF; antibody; cytostatic; anabolic;
KW eating-disorders-gen; immunomodulator; antimicrobial; cardiovascular-gen;
KW neuroprotective; gene; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .327
FT /*tag= a
FT /partial
FT /product= "9C1A light chain variable region"
FT /note= "No start or stop codon"
XX
PN WO2003083061-A2.
XX
PD 09-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009072.
XX
PR 26-MAR-2002; 2002US-0367903P.
XX
PA (CENZ) CENTOCOR INC.
XX
PI Giles-Komar J, Scallon BJ, Carton JM;
XX
DR WPI; 2003-804040/75.
DR P-PSDB; ADD89870.
XX
PT New isolated mammalian anti-tumor necrosis factor (TNF) antibody, useful
PT for diagnosing or treating an anti-TNF related condition, e.g. cancer,
PT anorexia, cachexia, or bacterial infection.
XX
PS Example 4; Fig 3A; 87pp; English.
XX
CC The present sequence is the coding sequence of the light chain variable
CC region of human anti-tumour necrosis factor (TNF) monoclonal antibody
CC 9C1A. This human TNF reactive IgG monoclonal antibody was generated by
CC cloning variable and constant region DNA in vector pC4 and expression in
CC CHO cells. The invention provides isolated human, primate, rodent,
CC mammalian, chimeric, humanized and/or CDR-grafted anti-TNF antibodies,
CC immunoglobulins, their cleavage products, other specified portions and
CC variants, as well as anti-TNF antibody compositions, nucleic acids
CC encoding these, vectors, host cells, methods for producing the antibodies
CC using a host cell, transgenic animal or transgenic plant or plant cell,
CC and therapeutic compositions, methods and devices. The antibody, nucleic
CC acid, protein, composition and methods are useful for diagnosing or
CC treating an anti-TNF related condition, e.g. cancer, anorexia, cachexia,
CC or an immune, cardiovascular, infectious, and/or neurological disease.
XX
SQ Sequence 327 BP; 84 A; 89 C; 76 G; 78 T; 0 U; 0 Other;

Query Match 74.3%; Score 238.6; DB 10; Length 327;
Best Local Similarity 84.5%; Pred. No. 6.7e-67;
Matches 268; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

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Qy          5 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 TCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64

Qy         65 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGAC 124
              |||||||||||||||| |||||||||    ||||   ||||||||||||||||||||
Db         65 CTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGA 124

Qy        125 AGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGAT 184
              | |||||||||| || || ||    || || |    ||||   ||||||||     | |
Db        125 AAGCTCCTAAGCTCCTGATCTATGATGCCTCCTATTTGGAAAGTGGGGTCCCATCAAGGT 184

Qy        185 TCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244
              |||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||||
Db        185 TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244

Qy        245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGA 304
              ||||||| ||||| |  |||||||||| | | ||||  ||||||||||||||||||||||
Db        245 ATTTTGCAACTTATTACTGTCAACAGTTTAAAAGTTACCCGATCACCTTCGGCCAAGGGA 304

Qy        305 CACGACTGGACATTCAA 321
              ||||||||| ||| ||
```

```
Db        305 CACGACTGGAGATTAAA 321

RESULT 15
ADP22249
ID   ADP22249 standard; cDNA; 321 BP.
XX
AC   ADP22249;
XX
DT   09-SEP-2004  (first entry)
XX
DE   Human anti-TNFa antibody light chain variable region cDNA SEQ ID NO:155.
XX
KW   human; monoclonal antibody; tumour necrosis factor-alpha; TNFa;
KW   anti-TNFa antibody; anabolic; antiarteriosclerotic; antiarthritic;
KW   antibacterial; antiinflammatory; antipsoriatic; antirheumatic;
KW   eating-disorder; immunomodulator; immunosuppressive; nephrotropic;
KW   neuroprotective; vasotropic; antiapoptotic; TNFa antagonist;
KW   TNF induced apoptosis; neoplastic disease; breast cancer; ovarian cancer;
KW   bladder cancer; lung cancer; glioblastoma; stomach cancer;
KW   endometrial cancer; kidney cancer; colon cancer; pancreatic cancer;
KW   prostrate cancer; immuno-mediated inflammatory disease;
KW   rheumatoid arthritis; glomerulonephritis; atherosclerosis; psoriasis;
KW   restenosis; autoimmune disease; Crohn's disease; graft-host reaction;
KW   septic shock; cachexia; anorexia; multiple sclerosis; gene; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .321
FT                   /*tag= a
FT                   /product= "human anti-TNFa antibody light chain variable
FT                   region"
XX
PN   WO2004050683-A2.
XX
PD   17-JUN-2004.
XX
PF   02-DEC-2003; 2003WO-US038281.
XX
PR   02-DEC-2002; 2002US-0430729P.
XX
PA   (ABGE-) ABGENIX INC.
XX
PI   Babcook JS,  Kang JS,  Foord O,  Green L,  Feng X,  Klakamp S;
PI   Haak-Frendscho M,  Rathanaswami P,  Pigott C,  Liang ML,  Lee R;
PI   Manchulencho K,  Faggioni R,  Senaldi G,  Qiaojuan JS;
XX
DR   WPI; 2004-480601/45.
DR   P-PSDB; ADP22250.
XX
PT   New recombinant human monoclonal antibody that specifically binds to
PT   Tumor Necrosis Factor-alpha, useful for treating neoplastic disease such
PT   as cancers, or immuno-mediated inflammatory diseases such as rheumatoid
PT   arthritis.
XX
PS   Example 10; SEQ ID NO 155; 213pp; English.
XX
CC   The present invention describes a human monoclonal antibody (I) that
CC   specifically binds to tumour necrosis factor-alpha (TNFa) and comprises:
CC   (a) a heavy chain complementarity determining region 1 (CDR1) having the
CC   two fully defined 5 amino acid sequence (S1, ADP22417) or (S2, ADP22421);
CC   and (b) a light chain CDR1 having the two fully defined 11 amino acid
CC   sequence (S3, ADP22418) or (S4, ADP22424). Also described: (1) assaying
CC   (M1) the level of TNFa in a patient sample, comprising contacting with
CC   (I), and detecting the level of binding between the antibody and TNFa in
CC   the sample; (2) a composition comprising the antibody or its functional
CC   fragment and a carrier; (3) treating (M2) an animal suffering from a
CC   neoplastic, or an immuno-mediated inflammatory disease by selecting an
CC   animal in need of treatment for the disease by administering the human
CC   monoclonal antibody of (I); and (4) inhibiting (M3) TNFa induced
CC   apoptosis in an animal by selecting an animal in need of treatment for
CC   TNFa induced apoptosis by administering the human monoclonal antibody of
CC   (I). (I) has anabolic, antiarteriosclerotic, antiarthritic,
CC   antibacterial, antiinflammatory, antipsoriatic, antirheumatic, eating-
CC   disorders, immunomodulator, immunosuppressive, nephrotropic,
CC   neuroprotective, vasotropic and antiapoptotic activities, and can be used
CC   as a TNFa antagonist. The antibody (I) is useful in the preparation of
CC   medicament for treating TNF induced apoptosis, neoplastic disease such as
CC   breast cancer, ovarian cancer, bladder cancer, lung cancer, glioblastoma,
CC   stomach cancer, endometrial cancer, kidney cancer, colon cancer,
CC   pancreatic cancer, and prostrate cancer; or immuno-mediated inflammatory
CC   diseases such as rheumatoid arthritis, glomerulonephritis,
CC   atherosclerosis, psoriasis, restenosis, autoimmune disease, Crohn's
CC   disease, graft-host reactions, septic shock, cachexia, anorexia, and
CC   multiple sclerosis. The present sequence encodes a human anti-TNFa
CC   antibody light chain variable region, which is used in the
CC   exemplification of the present invention.
XX
SQ   Sequence 321 BP; 87 A; 88 C; 71 G; 75 T; 0 U; 0 Other;

  Query Match             74.1%;  Score 237.8;  DB 12;  Length 321;
  Best Local Similarity   83.8%;  Pred. No. 1.2e-66;
  Matches  269;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGACAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||| || | || || ||    ||||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTGAGGTCCTGATCTATGCTGCATCCAATTTGCAACGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||| |||||||  |||||||||  |  ||||   |  ||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTCCAGTACCCTCATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


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GenCore version 5.1.6

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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	240.8	75.0	321	3	US-09-240-274-106	Sequence 106, App
2	236.2	73.6	321	2	US-08-378-939-13	Sequence 13, Appl
3	231.4	72.1	720	4	US-09-192-854-1	Sequence 1, Appli
4	228.2	71.1	714	4	US-09-472-087-62	Sequence 62, Appl
5	224	69.8	321	3	US-09-240-274-216	Sequence 216, App
6	223.2	69.5	321	3	US-09-240-274-102	Sequence 102, App
7	223.2	69.5	321	3	US-09-240-274-109	Sequence 109, App
8	223.2	69.5	321	3	US-09-240-274-215	Sequence 215, App
9	223.2	69.5	321	3	US-09-240-274-217	Sequence 217, App
10	223.2	69.5	321	3	US-09-240-274-218	Sequence 218, App
11	221.6	69.0	321	3	US-09-240-274-199	Sequence 199, App
12	220.2	68.6	388	3	US-09-042-353-358	Sequence 358, App
13	220.2	68.6	388	3	US-08-758-417A-206	Sequence 206, App
14	220	68.5	321	3	US-09-240-274-107	Sequence 107, App
15	218.4	68.0	321	3	US-09-240-274-211	Sequence 211, App
16	218.4	68.0	321	3	US-09-240-274-221	Sequence 221, App
17	218.4	68.0	321	3	US-09-240-274-222	Sequence 222, App
18	217.8	67.9	451	4	US-09-472-087-50	Sequence 50, Appl
19	217	67.6	439	3	US-09-042-353-360	Sequence 360, App
20	217	67.6	439	3	US-08-758-417A-208	Sequence 208, App
21	216.8	67.5	321	3	US-09-240-274-201	Sequence 201, App
22	216.2	67.4	672	4	US-09-456-090A-47	Sequence 47, Appl
23	216.2	67.4	672	4	US-09-453-234-47	Sequence 47, Appl
24	216	67.3	321	3	US-09-240-274-205	Sequence 205, App
25	215.4	67.1	324	2	US-08-378-939-31	Sequence 31, Appl
26	215.4	67.1	324	2	US-08-378-939-33	Sequence 33, Appl
27	215.4	67.1	387	3	US-08-803-085-3	Sequence 3, Appli
28	215.4	67.1	19040	4	US-09-343-485A-3	Sequence 3, Appli
29	215.2	67.0	321	3	US-09-240-274-105	Sequence 105, App
30	215.2	67.0	321	3	US-09-240-274-113	Sequence 113, App
31	213.8	66.6	324	2	US-08-378-939-17	Sequence 17, Appl
32	213.8	66.6	420	3	US-09-042-353-420	Sequence 420, App
33	213.8	66.6	420	3	US-08-758-417A-220	Sequence 220, App
34	213.8	66.6	3819	3	US-09-042-353-393	Sequence 393, App
35	213.8	66.6	3819	3	US-08-758-417A-243	Sequence 243, App
36	213.6	66.5	321	3	US-09-240-274-108	Sequence 108, App
37	213.6	66.5	321	3	US-09-240-274-203	Sequence 203, App
38	213.6	66.5	402	4	US-09-472-087-49	Sequence 49, Appl
39	213.2	66.4	390	2	US-08-646-367-2	Sequence 2, Appli
40	212.2	66.1	321	1	US-08-488-376-12	Sequence 12, Appl
41	212.2	66.1	321	2	US-08-634-223-12	Sequence 12, Appl
42	212.2	66.1	321	2	US-08-634-224-12	Sequence 12, Appl
43	212.2	66.1	321	2	US-08-634-400-12	Sequence 12, Appl
44	212.2	66.1	321	2	US-08-635-878-12	Sequence 12, Appl
45	212.2	66.1	321	2	US-08-770-057-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-240-274-106
; Sequence 106, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
; APPLICANT: Siegel, Donald L.
; TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
; TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
; FILE REFERENCE: 09596-42U2
; CURRENT APPLICATION NUMBER: US/09/240,274
; CURRENT FILING DATE: 1999-01-29
; EARLIER APPLICATION NUMBER: 60/081,380
; EARLIER FILING DATE: 1998-04-10
; EARLIER APPLICATION NUMBER: 60/028,550
; EARLIER FILING DATE: 1996-10-11
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
; LENGTH: 321
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: anti-Rh(D) chain I06
US-09-240-274-106

Query Match 75.0%; Score 240.8; DB 3; Length 321;
Best Local Similarity 85.1%; Pred. No. 1.1e-72;
Matches 269; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

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Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | |||||||| || || ||     ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||||  | |||||   ||||||||||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
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                ||||||||| ||| ||
Db        303 ACGACTGGAGATTAAA 318


RESULT 2
US-08-378-939-13
; Sequence 13, Application US/08378939
; Patent No. 5876961
;  GENERAL INFORMATION:
;    APPLICANT:  CROWE, JAMES SCOTT
;    APPLICANT:  LEWIS, ALAN PETER
;    TITLE OF INVENTION:  PRODUCTION OF ANTIBODIES
;    NUMBER OF SEQUENCES:  46
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  ROTHWELL, FIGG, ERNST & KURZ
;      STREET:  555 THIRTEENTH ST. N.W.
;      CITY:  WASHINGTON
;      STATE:  D. C.
;      COUNTRY:  U.S.
;      ZIP:  20004
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/378,939
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/952640
;      FILING DATE:  01-DEC-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  ERNST, BARBARA G
;      REGISTRATION NUMBER:  30,377
;      REFERENCE/DOCKET NUMBER:  1808-118
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202) 783-6040
;      TELEFAX:  (202) 783-6031
;  INFORMATION FOR SEQ ID NO:  13:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  321 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  both
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..321
US-08-378-939-13

  Query Match             73.6%;  Score 236.2;  DB 2;  Length 321;
  Best Local Similarity   83.5%;  Pred. No. 4e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||  ||||||||||||||||| |||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAATTATTTAAATTGGTATCAACAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||    |||||  |    | ||   ||||||  |
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCACATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||  ||||||| |||||||||| | | ||||||||||||||||||  ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGACTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||  ||| |||||||  |||||||||  | |||||    | ||||||||||||||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 3
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. 6696245
; GENERAL INFORMATION:
;  APPLICANT: Winter, Greg
;  APPLICANT: Tomlinson, Ian
;  TITLE OF INVENTION: Methods for Selecting Functional Peptides
;  FILE REFERENCE: 3789/72916
;  CURRENT APPLICATION NUMBER: US/09/192,854
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/066,729
;  EARLIER FILING DATE: 1997-11-21
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-192-854-1

  Query Match             72.1%;  Score 231.4;  DB 4;  Length 720;
  Best Local Similarity   82.6%;  Pred. No. 2.6e-69;
  Matches  265;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||    |||||  |    | ||   ||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||  ||||||| |||||||||| ||| ||||||||||||||||||  ||||| |||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||| |||||||  |||||||||  | |||||   || |  || |||||||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||      |||| ||  ||
Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 4
US-09-472-087-62
; Sequence 62, Application US/09472087
; Patent No. 6682736
; GENERAL INFORMATION:
;  APPLICANT: HANSON, DOUGLAS C.
;  APPLICANT:  NEVEU, MARK J.
;  APPLICANT:  MUELLER, EILLEN E.
;  APPLICANT:  HANKE, JEFFREY H.
;  APPLICANT:  GILMAN, STEVEN C.
;  APPLICANT:  DAVIS, C. GEOFFREY
;  APPLICANT:  CORVALAN, JOSE R.
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
;  FILE REFERENCE: ABX-PF1
```

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;  CURRENT APPLICATION NUMBER: US/09/472,087
;  CURRENT FILING DATE:  1999-12-23
;  PRIOR APPLICATION NUMBER: 60/113,647
;  PRIOR FILING DATE: 1998-12-23
;  NUMBER OF SEQ ID NOS: 147
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
;   LENGTH: 714
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-472-087-62

  Query Match             71.1%;  Score 228.2;  DB 4;  Length 714;
  Best Local Similarity   81.9%;  Pred. No. 3.2e-68;
  Matches  263;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||| |||||||||| ||||||||||||||||||||
Db        127 ATCACTTGCCGGGCAAGTCAGAGCATTAACAGCTATTTAGATTGGTATCAGCAGAAACCA 186

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||| || || || ||    ||||| |    | ||   ||||||||
Db        187 GGGAAAGCCCCTAAACTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| |||
Db        247 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 306

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||| | |||||   ||  |||| |||||||
Db        307 GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTTCGGCCCT 366

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||   | |||| ||  ||
Db        367 GGGACCAAAGTGGAAATCAAA 387


RESULT 5
US-09-240-274-216
; Sequence 216, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 216
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH47
US-09-240-274-216

  Query Match             69.8%;  Score 224;  DB 3;  Length 321;
  Best Local Similarity   82.4%;  Pred. No. 6.1e-67;
  Matches  257;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              ||||||||||||||||||||||||| |||||||||||||||||||||||||||||| |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCAGGAAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | ||||| || || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAACCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||||  | ||||||  ||   ||| ||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTTATCCTCGCACGTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACAT 317
              |||| ||
Db        303 CAAGGTGGAGAT 314


RESULT 6
US-09-240-274-102
; Sequence 102, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 102
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I02
US-09-240-274-102

  Query Match             69.5%;  Score 223.2;  DB 3;  Length 321;
  Best Local Similarity   81.6%;  Pred. No. 1.1e-66;
  Matches  258;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | ||||||||  || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||||  | ||||  | |   || |||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCTGTGGACGTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
              |||| ||  ||
```

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Db        303 CAAGGTGGAAATCAAA 318


RESULT 7
US-09-240-274-109
; Sequence 109, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 109
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I09
US-09-240-274-109

  Query Match            69.5%;  Score 223.2;  DB 3;  Length 321;
  Best Local Similarity  81.6%;  Pred. No. 1.1e-66;
  Matches  258;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | ||||-|||| || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| ||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTCCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| ||||| |  |||||||||  | | ||||  |||  ||| || ||||| |||||
Db        243 TTTTGCAACTTATTACTGTCAACAGCTTAATAGTTACCCGTACACTTTTGGCCAGGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                  ||||| ||  ||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 8
US-09-240-274-215
; Sequence 215, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 215
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH46
US-09-240-274-215

  Query Match            69.5%;  Score 223.2;  DB 3;  Length 321;
  Best Local Similarity  81.6%;  Pred. No. 1.1e-66;
  Matches  258;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||  |||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGTACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
                | ||||| || || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAATCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| ||||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| ||||||| |||||||||| || ||||||  || | ||| |||||||  |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGACTTACAGTTCCCCTAGCACTTTCGGCCCTGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                  ||||| ||  ||
Db        303 CAAAGTGGATATCAAA 318


RESULT 9
US-09-240-274-217
; Sequence 217, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 217
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH48
US-09-240-274-217

  Query Match            69.5%;  Score 223.2;  DB 3;  Length 321;
  Best Local Similarity  81.6%;  Pred. No. 1.1e-66;
  Matches  258;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||  |||||||||||||||||||||||||||||||||||||||  |
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Db         63 TTGCCGGGCAAGTCAGTACATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | ||||| || || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAATCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||| || ||||||  || | ||| |||||||  |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGACTTACAGTTCCCCTAGCACTTTCGGCCCTGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                | |||| ||  ||
Db        303 CAAAGTGGATATCAAA 318


RESULT 10
US-09-240-274-218
; Sequence 218, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 218
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH49
US-09-240-274-218

  Query Match             69.5%;  Score 223.2;  DB 3;  Length 321;
  Best Local Similarity   81.6%;  Pred. No. 1.1e-66;
  Matches  258;  Conservative    0;  Mismatches   58;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCGTCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||| | |||||   |||   || ||||||||||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                |||| ||  ||
Db        303 CAAGGTGGAAATCAAA 318


RESULT 11
US-09-240-274-199
; Sequence 199, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 199
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH13
US-09-240-274-199

  Query Match             69.0%;  Score 221.6;  DB 3;  Length 321;
  Best Local Similarity   81.3%;  Pred. No. 4e-66;
  Matches  257;  Conservative    0;  Mismatches   59;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | ||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||   |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||    ||||| |    | |   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCGAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||| | |||||   ||   ||| || ||||| |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCCTACACTTTTGGCCAGGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                |||| ||  ||
Db        303 CAAGCTGGAGATCAAA 318


RESULT 12
US-09-042-353-358
; Sequence 358, Application US/09042353
; Patent No. 6255458
;  GENERAL INFORMATION:
;    APPLICANT:  Lonberg, Nils
;    APPLICANT:  Kay, Robert M.
;    TITLE OF INVENTION:  Transgenic No. 6255458-Human Animals for
;    TITLE OF INVENTION:  Producing Heterologous Antibodies
;    NUMBER OF SEQUENCES:  421
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Townsend and Townsend and Crew LLP
;      STREET:  Two Embarcadero Center, Eighth Floor
;      CITY:  San Francisco
;      STATE:  California
;      COUNTRY:  USA
;      ZIP:  94111-3834
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/042,353
;      FILING DATE:  13-MAR-1998
;      CLASSIFICATION:  800
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/810,279
;      FILING DATE:  17-DEC-1991
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/853,408
;      FILING DATE:  18-MAR-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/904,068
;      FILING DATE:  23-JUN-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/990,860
;      FILING DATE:  16-DEC-1992
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/053,131
;      FILING DATE:  26-APR-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/096,762
;      FILING DATE:  22-JUL-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/155,301
;      FILING DATE:  18-NOV-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/161,739
;      FILING DATE:  03-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/165,699
;      FILING DATE:  10-DEC-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/209,741
;      FILING DATE:  09-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/352,322
;      FILING DATE:  07-DEC-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/544,404
;      FILING DATE:  10-OCT-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/728,463
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US96/16433
;      FILING DATE:  10-OCT-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/758,417
;      FILING DATE:  02-DEC-1996
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US97/21803
;      FILING DATE:  01-DEC-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Apple, Randolph T.
;      REGISTRATION NUMBER:  36,429
;      REFERENCE/DOCKET NUMBER:  014643-009040US
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 576-0200
;      TELEFAX:  (415) 576-0300
;  INFORMATION FOR SEQ ID NO:  358:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  388 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA
US-09-042-353-358

  Query Match             68.6%;  Score 220.2;  DB 3;  Length 388;
  Best Local Similarity   80.4%;  Pred. No. 1.3e-65;

  Matches  258;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||| ||||||   |||||||||| |||   |||||||||| ||||||
Db        127 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||    ||||| |    | ||   ||||||||
Db        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||||||||||| |||||||||| ||| ||||||||||||||||||||||||||
Db        247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| ||||||| |||||||||| || | ||||| |||  ||| || |||||
Db        307 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        367 GGGACCAAGCTGGAGATCAAA 387


RESULT 13
US-08-758-417A-206
; Sequence 206, Application US/08758417A
; Patent No. 6300129
;   GENERAL INFORMATION:
;        APPLICANT: Lonberg, Nils
;                   Kay, Robert M.
;        TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for
;                            Producing Heterologous Antibodies
;        NUMBER OF SEQUENCES: 417
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Townsend and Townsend and Crew LLP
;             STREET: Two Embarcadero Center, Eighth Floor
;             CITY: San Francisco
;             STATE: California
;             COUNTRY: USA
;             ZIP: 94111-3834
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/08/758,417A
;             FILING DATE: 02-Dec-1996
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US 08/728,463
;             FILING DATE: 10-OCT-1996
;             APPLICATION NUMBER: US 08/544,404
;             FILING DATE: 10-OCT-1995
;             APPLICATION NUMBER: US 08/352,322
;             FILING DATE: 07-DEC-1994
;             APPLICATION NUMBER: US 08/209,741
;             FILING DATE: 09-MAR-1994
;             APPLICATION NUMBER: US 08/165,699
;             FILING DATE: 10-DEC-1993
;             APPLICATION NUMBER: US 08/161,739
;             FILING DATE: 03-DEC-1993
;             APPLICATION NUMBER: US 08/155,301
;             FILING DATE: 18-NOV-1993
;             APPLICATION NUMBER: US 08/096,762
;             FILING DATE: 22-JUL-1993
;             APPLICATION NUMBER: US 08/053,131
;             FILING DATE: 26-APR-1993
;             APPLICATION NUMBER: US 07/990,860
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;            FILING DATE: 16-DEC-1992
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Serafini, Andrew T.
;            REGISTRATION NUMBER: 41,303
;            REFERENCE/DOCKET NUMBER: 014643-009030US
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (415) 576-0200
;            TELEFAX: (415) 576-0300
;   INFORMATION FOR SEQ ID NO: 206:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 388 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       MOLECULE TYPE: DNA
;       SEQUENCE DESCRIPTION: SEQ ID NO: 206:
US-08-758-417A-206

  Query Match            68.6%;  Score 220.2;  DB 3;  Length 388;
  Best Local Similarity  80.4%;  Pred. No. 1.3e-65;
  Matches  258;  Conservative    0;  Mismatches   63;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db         67 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 126

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||| ||||||   |||||||||| |||   |||||||||||| ||||||
Db        127 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCATAAACCA 186

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||    ||||| |    | ||   ||||||||
Db        187 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 246

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | |||||||||||||| |||||||||| ||| ||||||||||||||||||||||||||
Db        247 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 306

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||| ||||||| |||||||||| || | ||||| |||   ||| || |||||
Db        307 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAATAGTTTCCCGTACACTTTTGGCCAG 366

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        367 GGGACCAAGCTGGAGATCAAA 387


RESULT 14
US-09-240-274-107
; Sequence 107, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 107
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I07
US-09-240-274-107

  Query Match            68.5%;  Score 220;  DB 3;  Length 321;
  Best Local Similarity  81.0%;  Pred. No. 1.4e-65;
  Matches  256;  Conservative    0;  Mismatches   60;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 AGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||| | |||||   ||    || ||||||  ||||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCGAACTTTCGGCGGAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                  |||| ||  ||
Db        303 CAAGGTGGAGATCAAA 318


RESULT 15
US-09-240-274-211
; Sequence 211, Application US/09240274
; Patent No. 6255455
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION: SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/240,274
;  CURRENT FILING DATE: 1999-01-29
;  EARLIER APPLICATION NUMBER: 60/081,380
;  EARLIER FILING DATE: 1998-04-10
;  EARLIER APPLICATION NUMBER: 60/028,550
;  EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 211
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) antibody clone SH36
US-09-240-274-211

  Query Match            68.0%;  Score 218.4;  DB 3;  Length 321;
  Best Local Similarity  80.7%;  Pred. No. 5e-65;
  Matches  255;  Conservative    0;  Mismatches   61;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65
              | || | || ||||||||||||||||||||||||||||||||||||||||||||||||||
Db          3 CGAGCTCACTCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  |
Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185
              | |||||||| || || ||    ||||| |    | ||   ||||||||     | ||
Db        123 ATCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245
              ||| ||||||| |||||||||| ||| |||||||||||||||| ||||| ||||||||
Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242
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Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305
              |||||| |||||||  |||||||||  | |||||    ||     | |||||||  |||||
Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTCCGGCTTTCGGCCCTGGGAC 302

Qy        306 ACGACTGGACATTCAA 321
                | |||| ||  ||
Db        303 CAAAGTGGATATCAAA 318
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Search completed: December 7, 2004, 08:57:56
Job time : 67.271 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 08:53:09 ; Search time 275.899 Seconds
(without alignments)
6393.344 Million cell updates/sec

Title: US-09-403-107-147
Perfect score: 321
Sequence: 1 gagctccagatgacccagtc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3695051 seqs, 2747533894 residues

Total number of hits satisfying chosen parameters: 7390102

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	321	100.0	321	15	US-10-325-694-147	Sequence 147, App
2	255.4	79.6	321	15	US-10-325-694-141	Sequence 141, App
3	245.8	76.6	324	17	US-10-344-514-7	Sequence 7, Appli
4	245.8	76.6	324	17	US-10-344-514-8	Sequence 8, Appli
5	240.8	75.0	321	10	US-09-848-798-106	Sequence 106, App
6	240.2	74.8	321	17	US-10-703-714-11	Sequence 11, Appl
7	240.2	74.8	321	17	US-10-703-714-19	Sequence 19, Appl
8	239.4	74.6	322	16	US-10-309-762-215	Sequence 215, App
9	239.4	74.6	322	16	US-10-309-762-228	Sequence 228, App
10	236.2	73.6	322	16	US-10-309-762-213	Sequence 213, App
11	236.2	73.6	322	16	US-10-309-762-238	Sequence 238, App
12	235	73.2	1106	16	US-10-264-049-121	Sequence 121, App
13	231.4	72.1	333	15	US-10-203-754A-60	Sequence 60, Appl
14	231.4	72.1	720	9	US-09-192-854-1	Sequence 1, Appli
15	231.4	72.1	720	9	US-09-968-561A-1	Sequence 1, Appli
16	231.4	72.1	720	10	US-09-968-744A-1	Sequence 1, Appli
17	231.4	72.1	720	11	US-09-968-561A-1	Sequence 1, Appli
18	231.4	72.1	720	18	US-10-744-774-2	Sequence 2, Appli
19	231.4	72.1	900	15	US-10-203-754A-64	Sequence 64, Appl
20	229.8	71.6	321	16	US-10-338-366-11	Sequence 11, Appl
21	229.8	71.6	324	17	US-10-344-514-3	Sequence 3, Appli
22	229.8	71.6	324	17	US-10-344-514-4	Sequence 4, Appli
23	229.8	71.6	729	15	US-10-216-484-125	Sequence 125, App
24	229.8	71.6	729	15	US-10-384-933-125	Sequence 125, App
25	228.2	71.1	322	16	US-10-309-762-226	Sequence 226, App
26	228.2	71.1	322	16	US-10-309-762-227	Sequence 227, App
27	228.2	71.1	324	18	US-10-409-814A-3	Sequence 3, Appli
28	228.2	71.1	714	14	US-10-153-382-18	Sequence 18, Appl
29	228.2	71.1	714	18	US-10-612-497-62	Sequence 62, Appl
30	228.2	71.1	714	18	US-10-776-649-62	Sequence 62, Appl
31	228.2	71.1	819	14	US-10-158-646-65	Sequence 65, Appl
32	226.6	70.6	322	15	US-10-041-860-74	Sequence 74, Appl
33	226.6	70.6	322	16	US-10-309-762-221	Sequence 221, App
34	226.6	70.6	322	16	US-10-309-762-233	Sequence 233, App
35	226.6	70.6	322	17	US-10-665-383-43	Sequence 43, Appl
36	226.6	70.6	463	16	US-10-395-894-20	Sequence 20, Appl
37	226.6	70.6	463	17	US-10-695-667-20	Sequence 20, Appl
38	226.6	70.6	514	14	US-10-066-543-2025	Sequence 2025, Ap
c 39	226.6	70.6	537	14	US-10-066-543-186	Sequence 186, App
40	226.6	70.6	6082	16	US-10-395-894-9	Sequence 9, Appli
41	226.6	70.6	6082	17	US-10-695-667-9	Sequence 9, Appli
42	225.8	70.3	321	14	US-10-073-644C-3	Sequence 3, Appli
43	225.4	70.2	322	16	US-10-038-591-54	Sequence 54, Appl
44	225.4	70.2	322	18	US-10-775-444A-54	Sequence 54, Appl
45	225	70.1	321	15	US-10-091-300-42	Sequence 42, Appl

ALIGNMENTS

RESULT 1
US-10-325-694-147
; Sequence 147, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
; APPLICANT: KUFER, PETER
; APPLICANT: RAUM, TOBIAS
; TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
; TITLE OF INVENTION: RECEPTORS AND USES THEREOF
; FILE REFERENCE: 38164000
; CURRENT APPLICATION NUMBER: US/10/325,694
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US/09/403,107
; PRIOR FILING DATE: 1999-10-14
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 147
; LENGTH: 321
; TYPE: DNA
; ORGANISM: HUMAN
US-10-325-694-147

Query Match 100.0%; Score 321; DB 15; Length 321;
Best Local Similarity 100.0%; Pred. No. 2.9e-101;
Matches 321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
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Db        301 GGGACACGACTGGACATTCAA 321


RESULT 2
US-10-325-694-141
; Sequence 141, Application US/10325694
; Publication No. US20030148463A1
; GENERAL INFORMATION:
;  APPLICANT: KUFER, PETER
;  APPLICANT:  RAUM, TOBIAS
;  TITLE OF INVENTION: NOVEL METHOD FOR THE PRODUCTION OF ANTI-HUMAN ANTIGEN
;  TITLE OF INVENTION:  RECEPTORS AND USES THEREOF
;  FILE REFERENCE: 38164000
;  CURRENT APPLICATION NUMBER: US/10/325,694
;  CURRENT FILING DATE:  2002-12-19
;  PRIOR APPLICATION NUMBER: US/09/403,107
;  PRIOR FILING DATE: 1999-10-14
;  NUMBER OF SEQ ID NOS: 152
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 141
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: HUMAN
US-10-325-694-141

  Query Match             79.6%;  Score 255.4;  DB 15;  Length 321;
  Best Local Similarity   87.2%;  Pred. No. 2.2e-78;
  Matches  280;  Conservative    0;  Mismatches   41;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||||||||||||||||||||||||||||||||||||||| ||||| ||||||||||||||||
Db          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTGGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||| ||||||||||||||||||||||| ||||||||||||||||||||||||
Db         61 ATCACTTGTCGGACAAGTCAGAGCATTAGCAGCTATTAAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              |||||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||
Db        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGCGATCTACCCGGGAATCCGGGGTCCCTGAC 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              |||||||| ||||| |  ||||||||| ||| |||||||||||||||||| || || |||
Db        181 CGATTCAGTGGCAGCGGGTCTGGGACAGATTTCACTCTCACCATCAGCAGTCTACAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||| ||| |||||||  ||||| |||  | ||    | |||  ||| || |||||
Db        241 GAAGATTCTGCAACTTACTACTGTCAGCAGAGTTACGACATCCCGTACACTTTTGGCCAG 300

Qy        301 GGGACACGACTGGACATTCAA 321
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Db        301 GGGACCAAGCTGGAGATCAAA 321


RESULT 3
US-10-344-514-7
; Sequence 7, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
;  APPLICANT: NAKASHIMA, Toshihiro et al.
;  TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
;  FILE REFERENCE: 0020-5111P
;  CURRENT APPLICATION NUMBER: US/10/344,514
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: JP 2001-177640
;  PRIOR FILING DATE: 2001-06-12
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 7
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-344-514-7

  Query Match             76.6%;  Score 245.8;  DB 17;  Length 324;
  Best Local Similarity   85.4%;  Pred. No. 4.9e-75;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || ||    ||||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||   ||||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 4
US-10-344-514-8
; Sequence 8, Application US/10344514
; Publication No. US20040120951A1
; GENERAL INFORMATION:
;  APPLICANT: NAKASHIMA, Toshihiro et al.
;  TITLE OF INVENTION: HUMAN ANTI-FACTOR VIII ANTIBODY
;  FILE REFERENCE: 0020-5111P
;  CURRENT APPLICATION NUMBER: US/10/344,514
;  CURRENT FILING DATE:  2003-07-28
;  PRIOR APPLICATION NUMBER: JP 2001-177640
;  PRIOR FILING DATE: 2001-06-12
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 8
;   LENGTH: 324
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(324)
US-10-344-514-8

  Query Match             76.6%;  Score 245.8;  DB 17;  Length 324;
  Best Local Similarity   85.4%;  Pred. No. 4.9e-75;
  Matches  274;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
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Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180

Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240

Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300

Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321

Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 5
US-09-848-798-106
; Sequence 106, Application US/09848798
; Publication No. US20030040605A1
; GENERAL INFORMATION:
;  APPLICANT: Siegel, Donald L.
;  TITLE OF INVENTION: Rh(D)-BINDING PROTEINS AND MAGNETICALLY ACTIVATED CELL
;  TITLE OF INVENTION:  SORTING METHOD FOR PRODUCTION THEREOF
;  FILE REFERENCE: 09596-42U2
;  CURRENT APPLICATION NUMBER: US/09/848,798
;  CURRENT FILING DATE:  2001-05-04
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/240,274
;  PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-29
;  PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/028,550
;  PRIOR FILING DATE: EARLIER FILING DATE: 1996-10-11
;  NUMBER OF SEQ ID NOS: 224
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 106
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   OTHER INFORMATION: anti-Rh(D) chain I06
US-09-848-798-106

  Query Match             75.0%;  Score 240.8;  DB 10;  Length 321;
  Best Local Similarity   85.1%;  Pred. No. 2.7e-73;
  Matches  269;  Conservative    0;  Mismatches   47;  Indels    0;  Gaps    0;

Qy          6 CCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 65

Db          3 CGAGCTCACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCAC 62

Qy         66 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGACA 125

Db         63 TTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGGAA 122

Qy        126 GCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGATT 185

Db        123 AGCCCCTAAGCTCCTGATCTATGCCGCATCCAGTTTGCAAAGTGGGGTCCCATCAAGGTT 182

Qy        186 CAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAGA 245

Db        183 CAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCTGAAGA 242

Qy        246 TTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGAC 305

Db        243 TTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGATCACCTTCGGCCAAGGGAC 302

Qy        306 ACGACTGGACATTCAA 321

Db        303 ACGACTGGAGATTAAA 318


RESULT 6
US-10-703-714-11
; Sequence 11, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
;  APPLICANT: Huang, Haichun
;  APPLICANT:  Holmes, Steven
;  APPLICANT:  Mason, Sean
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
;  FILE REFERENCE: MXI-294
;  CURRENT APPLICATION NUMBER: US/10/703,714
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: 60/424803
;  PRIOR FILING DATE: 2002-11-07
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 11
;   LENGTH: 321
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(321)
US-10-703-714-11

  Query Match             74.8%;  Score 240.2;  DB 17;  Length 321;
  Best Local Similarity   84.9%;  Pred. No. 4.3e-73;
  Matches  269;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          5 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64

Db          5 TCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64

Qy         65 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGAC 124

Db         65 CTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGA 124

Qy        125 AGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGAT 184

Db        125 AAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT 184

Qy        185 TCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244

Db        185 TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244

Qy        245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGA 304

Db        245 ATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCGATCACCTTCGGCCAAGGGA 304

Qy        305 CACGACTGGACATTCAA 321

Db        305 CACGACTGGAGATTAAA 321


RESULT 7
US-10-703-714-19
; Sequence 19, Application US/10703714
; Publication No. US20040170630A1
; GENERAL INFORMATION:
;  APPLICANT: Huang, Haichun
;  APPLICANT:  Holmes, Steven
;  APPLICANT:  Mason, Sean
;  TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO HEPARANASE
;  FILE REFERENCE: MXI-294
;  CURRENT APPLICATION NUMBER: US/10/703,714
;  CURRENT FILING DATE:  2003-11-07
;  PRIOR APPLICATION NUMBER: 60/424803
;  PRIOR FILING DATE: 2002-11-07
;  NUMBER OF SEQ ID NOS: 64
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 19
;   LENGTH: 321
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;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)...(321)
US-10-703-714-19

  Query Match             74.8%;  Score 240.2;  DB 17;  Length 321;
  Best Local Similarity   84.9%;  Pred. No. 4.3e-73;
  Matches  269;  Conservative    0;  Mismatches   48;  Indels    0;  Gaps    0;

Qy          5 TCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          5 TCCAGTTGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACCATCA 64

Qy         65 CTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCAGGAC 124
              |||||||||||||||| ||||||||||   ||||   ||||||||||||||||||||
Db         65 CTTGCCGGGCAAGTCAGGGCATTAGCAGTGCTTTAGCCTGGTATCAGCAGAAACCAGGGA 124

Qy        125 AGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGACCGAT 184
              |  |||||||||| || || ||    || || |    ||||   ||||||||      | |
Db        125 AAGCTCCTAAGCTCCTGATCTATGATGCCTCCAGTTTGGAAAGTGGGGTCCCATCAAGGT 184

Qy        185 TCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244
              |||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||||
Db        185 TCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCTGAAG 244

Qy        245 ATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAAGGGA 304
              |||||||  |||||  |  |||||||||| | | ||||  ||||||||||||||||||||
Db        245 ATTTTGCAACTTATTACTGTCAACAGTTTAATAGTTACCCGATCACCTTCGGCCAAGGGA 304

Qy        305 CACGACTGGACATTCAA 321
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Db        305 CACGACTGGAGATTAAA 321


RESULT 8
US-10-309-762-215
; Sequence 215, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 215
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-215

  Query Match             74.6%;  Score 239.4;  DB 16;  Length 322;
  Best Local Similarity   84.1%;  Pred. No. 8.3e-73;
  Matches  270;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||  |||||  ||||||  | |||||||  ||  ||||  ||||||||||||||||||
Db         61 ATCACTTGTCGGGCGAGTCAGGGTATTAGCATCTGGTTAACCTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||  || || ||    |||||  |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||
Db        181 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||  |||||||  |||||||||| || |||||||  || ||||||||||||||
Db        241 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 9
US-10-309-762-228
; Sequence 228, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 228
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-228

  Query Match             74.6%;  Score 239.4;  DB 16;  Length 322;
  Best Local Similarity   84.1%;  Pred. No. 8.3e-73;
  Matches  270;  Conservative    0;  Mismatches   51;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||  |||||  ||||||  | |||||||  ||  ||||  ||||||||||||||||||
Db         61 ATCACTTGTCGGGCGAGTCAGGGTATTAGCATCTGGTTAACCTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||  || || ||    |||||  |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||
Db        181 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||  |||||||  |||||||||| || |||||||  || ||||||||||||||
Db        241 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 10
US-10-309-762-213
; Sequence 213, Application US/10309762
; Publication No. US20040018198A1
```

```
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 213
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-213

  Query Match            73.6%;  Score 236.2;  DB 16;  Length 322;
  Best Local Similarity  83.5%;  Pred. No. 1.1e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||| | ||||||||||  |||   |||| ||||||||||||
Db         61 ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTTTCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | || ||||| || || ||    |||||  |    | ||   ||||||||
Db        121 GGGAAAGCCCCCAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||
Db        181 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| ||||||| |||||||||| || ||||||| || ||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 11
US-10-309-762-238
; Sequence 238, Application US/10309762
; Publication No. US20040018198A1
; GENERAL INFORMATION:
;  APPLICANT: Gudas, Jean
;  APPLICANT:  Foltz, Ian
;  APPLICANT:  Handa, Masahisa
;  APPLICANT:  Gallo, Michael
;  TITLE OF INVENTION: ANTIBODIES AGAINST CARBOXIC ANHYDRASE IX
;  TITLE OF INVENTION:  (CA IX) TUMOR ANTIGEN
;  FILE REFERENCE: ABGENIX.027A
;  CURRENT APPLICATION NUMBER: US/10/309,762
;  CURRENT FILING DATE:  2002-12-02
;  PRIOR APPLICATION NUMBER: 60/337275
;  PRIOR FILING DATE: 2001-12-03
;  NUMBER OF SEQ ID NOS: 246
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 238
;   LENGTH: 322
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-309-762-238

  Query Match            73.6%;  Score 236.2;  DB 16;  Length 322;
  Best Local Similarity  83.5%;  Pred. No. 1.1e-71;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||| | ||||||||||  |||   |||| ||||||||||||
Db         61 ATCACTTGTCGGGCGAGTCAGGGTATTAGCAGCTGGTTAGCCTGGTTTCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | || ||||| || || ||    |||||  |    | ||   ||||||||
Db        121 GGGAAAGCCCCCAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||||||||| |||||||||| ||| ||||||||||||||||||||||||||||
Db        181 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCCTGCAGCCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| ||||||| |||||||||| || ||||||| || ||||||||||||||||
Db        241 GAAGATTTTGCAACTTACTATTGTCAACAGGCTAACAGTTTCCCTATCACCTTCGGCCAA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        301 GGGACACGACTGGAGATTAAA 321


RESULT 12
US-10-264-049-121
; Sequence 121, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
;  APPLICANT: Birse et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PA133P1
;  CURRENT APPLICATION NUMBER: US/10/264,049
;  CURRENT FILING DATE:  2002-10-04
;  PRIOR APPLICATION NUMBER: PCT/US01/18569
;  PRIOR FILING DATE: 2001-06-07
;  PRIOR APPLICATION NUMBER: US 60/209,467
;  PRIOR FILING DATE: 2000-06-07
;  NUMBER OF SEQ ID NOS: 4360
;  SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 121
;   LENGTH: 1106
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (302)..(302)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (424)..(424)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1039)..(1039)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1084)..(1084)
;   OTHER INFORMATION: n equals a,t,g, or c
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1103)..(1103)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-264-049-121

  Query Match            73.2%;  Score 235;  DB 16;  Length 1106;
  Best Local Similarity  81.6%;  Pred. No. 4.6e-71;
```

```
  Matches  262;  Conservative    6;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        145 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 204

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        205 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAACTATTTAAATTGGTATCAGCAGAAACCA 264

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||| || || ||    ||||| |    | ||   ||||||||
Db        265 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCANTTTGCAAAGTGGGGTCCCATCA 324

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| |||||||| |||||||||| ||| ||||:|||||||||||||:|||||:|||
Db        325 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTYTCACCATCAGCAGYCTGCARCCT 384

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||:|  |||||||||| ||| | | | ||  |||| ||||||::|
Db        385 GAAGATTTTGCAACTTAYTACTGTCAACAGTATGATAATNTCCCTCTCACTTTCGGCSRA 444

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||     |||| || ||
Db        445 GGGACCAAGGTGGARATCAAA 465


RESULT 13
US-10-203-754A-60
; Sequence 60, Application US/10203754A
; Publication No. US20030157132A1
; GENERAL INFORMATION:
;  APPLICANT: ITAMI, Seima
;  APPLICANT:  SEKI, Makoto
;  APPLICANT:  MATSUURA, Yoshiharu
;  APPLICANT:  SHIBUI, Tatsurou
;  APPLICANT:  YOTSUMOTO, Yoshihisa
;  APPLICANT:  MIYAMURA, Tatsuo
;  TITLE OF INVENTION: Therapeutic Agent for Hepatitis C
;  FILE REFERENCE: P22257
;  CURRENT APPLICATION NUMBER: US/10/203,754A
;  CURRENT FILING DATE:  2002-08-13
;  PRIOR APPLICATION NUMBER: PCT/JP01/00967
;  PRIOR FILING DATE: 2001-02-13
;  NUMBER OF SEQ ID NOS: 81
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
;   LENGTH: 333
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-203-754A-60

  Query Match             72.1%;  Score 231.4;  DB 15;  Length 333;
  Best Local Similarity   82.6%;  Pred. No. 5.2e-70;
  Matches  265;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||| || || ||    ||||| |    | ||   ||||||||
Db        121 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 180

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| |||||||| |||||||||| ||| |||||||||||||||||| ||||| |||
Db        181 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 240

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||   ||| |||| ||||||  |
Db        241 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGCTCACTTTCGGCGGA 300

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||     |||| ||  ||
Db        301 GGGACCAAGGTGGAGATCAAA 321


RESULT 14
US-09-192-854-1
; Sequence 1, Application US/09192854
; Patent No. US20020068276A1
; GENERAL INFORMATION:
;  APPLICANT: Winter, Greg
;  APPLICANT: Tomlinson, Ian
;  TITLE OF INVENTION: Methods for Selecting Functional Peptides
;  FILE REFERENCE: 3789/72916
;  CURRENT APPLICATION NUMBER: US/09/192,854
;  CURRENT FILING DATE: 1998-11-17
;  EARLIER APPLICATION NUMBER: 60/066,729
;  EARLIER FILING DATE: 1997-11-21
;  NUMBER OF SEQ ID NOS: 212
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 720
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-192-854-1

  Query Match             72.1%;  Score 231.4;  DB 9;  Length 720;
  Best Local Similarity   82.6%;  Pred. No. 7e-70;
  Matches  265;  Conservative    0;  Mismatches   56;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||| || || ||    ||||| |    | ||   ||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| |||||||| |||||||||| ||| |||||||||||||||||| ||||| |||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||   || |  || |||||||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||     |||| ||  ||
Db        697 GGGACCAAGGTGGAAATCAAA 717


RESULT 15
US-09-968-561A-1
; Sequence 1, Application US/09968561A
; Patent No. US20020164642A1
; GENERAL INFORMATION:
;  APPLICANT: Tomlinson, Ian M
;  APPLICANT:  Winter, Gregory
;  TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
;  FILE REFERENCE: 8039/1073B
;  CURRENT APPLICATION NUMBER: US/09/968,561A
;  CURRENT FILING DATE:  2001-10-01
;  PRIOR APPLICATION NUMBER: GB 9722131.1
;  PRIOR FILING DATE: 1997-10-20
;  PRIOR APPLICATION NUMBER: US 60/065,248
;  PRIOR FILING DATE: 1997-11-13
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; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-561A-1

Query Match 72.1%; Score 231.4; DB 9; Length 720;
Best Local Similarity 82.6%; Pred. No. 7e-70;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

```
Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        397 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 456

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        457 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 516

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || ||    ||||| |    | ||   ||||||||
Db        517 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 576

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | ||||| ||||||| |||||||||| ||| |||||||||||||||| ||||| |||
Db        577 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 636

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||   || |  || |||||||||
Db        637 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAATACGTTCGGCCAA 696

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||     |||| ||  ||
Db        697 GGGACCAAGGTGGAAATCAAA 717
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Search completed: December 7, 2004, 14:26:31
Job time : 275.899 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: December 7, 2004, 06:11:35 ; Search time 1873.31 Seconds
(without alignments)
6244.126 Million cell updates/sec

Title: US-09-403-107-147
Perfect score: 321
Sequence: 1 gagctccagatgacccagtc.....ggacacgactggacattcaa 321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	238.4	74.3	353	2	AW404894	AW404894 UI-HF-BL0
2	237.8	74.1	794	6	CB955875	CB955875 AGENCOURT
3	236.2	73.6	621	4	BM171889	BM171889 imageqc_3
4	236.2	73.6	748	6	CB957070	CB957070 AGENCOURT
5	234.6	73.1	826	4	BG742662	BG742662 602633264
6	233	72.6	709	6	CD690167	CD690167 EST6690 h
7	233	72.6	781	6	CB985512	CB985512 AGENCOURT
8	231.6	72.1	553	6	CD705041	CD705041 EST21568
9	231.4	72.1	421	2	AW406227	AW406227 UI-HF-BL0
10	231.4	72.1	422	2	AW407904	AW407904 UI-HF-BL0
11	231.4	72.1	521	6	CD707755	CD707755 EST24282
12	231.4	72.1	587	4	BG756289	BG756289 602713607
13	231.4	72.1	624	6	CD690145	CD690145 EST6668 h
14	230.6	71.8	570	4	BG536784	BG536784 602566318
15	229.8	71.6	486	6	CD683960	CD683960 EST480 hu
16	229.8	71.6	493	2	AW405753	AW405753 UI-HF-BL0
17	229.8	71.6	797	6	CB987347	CB987347 AGENCOURT
18	229.8	71.6	831	6	CB987031	CB987031 AGENCOURT
19	228.2	71.1	525	6	CD705928	CD705928 EST22455
20	228.2	71.1	708	6	CB956923	CB956923 AGENCOURT
21	228.2	71.1	773	4	BM007845	BM007845 603617528
22	227.4	70.8	339	1	AB107216	AB107216 AB107216
23	227.4	70.8	499	6	CD685478	CD685478 EST1998 h
24	226.6	70.6	487	2	AW405301	AW405301 UI-HF-BL0
25	226.6	70.6	559	4	BG547768	BG547768 602575646
26	226.6	70.6	693	6	CD684441	CD684441 EST961 hu
27	226.6	70.6	754	6	CB986767	CB986767 AGENCOURT
28	226.6	70.6	785	6	CB955817	CB955817 AGENCOURT
29	226.6	70.6	864	4	BG548281	BG548281 602575248
30	226.6	70.6	923	5	BQ882857	BQ882857 AGENCOURT
31	226.4	70.5	740	6	CB987627	CB987627 AGENCOURT
32	226.4	70.5	756	6	CB984720	CB984720 AGENCOURT
33	225.8	70.3	608	2	AW404714	AW404714 UI-HF-BL0
34	225.8	70.3	921	4	BG341239	BG341239 602463904
35	225	70.1	391	2	AW404992	AW404992 UI-HF-BL0
36	225	70.1	460	2	AW405906	AW405906 UI-HF-BL0
37	225	70.1	510	6	CD694557	CD694557 EST11080
38	225	70.1	550	6	CD709957	CD709957 EST26484
39	225	70.1	566	2	AW406081	AW406081 UI-HF-BL0
40	225	70.1	695	6	CD683876	CD683876 EST396 hu
41	225	70.1	724	6	CB959008	CB959008 AGENCOURT
42	225	70.1	742	6	CB984723	CB984723 AGENCOURT
43	225	70.1	759	6	CB986444	CB986444 AGENCOURT
44	225	70.1	785	6	CB986976	CB986976 AGENCOURT
45	225	70.1	820	6	CB956240	CB956240 AGENCOURT

ALIGNMENTS

RESULT 1
AW404894
LOCUS AW404894 353 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BL0-acn-f-07-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059844 5', mRNA sequence.
ACCESSION AW404894
VERSION AW404894.1 GI:6923951
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 353)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .353
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059844"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
ORIGIN

Query Match 74.3%; Score 238.4; DB 2; Length 353;
Best Local Similarity 85.3%; Pred. No. 5.5e-66;

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  Matches  266;  Conservative    0;  Mismatches   46;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db         42 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACC 101

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| | ||||||||||||||||||||||||||
Db        102 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGTTCTTTAAATTGGTATCAGCAGAAACCA 161

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||| ||| || || ||    ||||| |    | ||   ||||||||
Db        162 GGGAAAGCCCCTAGGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 221

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| |||
Db        222 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 281

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||||  | |||||| ||||||||||||||||||||
Db        282 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTTCGCCGATCACCTTCGGCCAA 341

Qy        301 GGGACACGACTG 312
              ||||||||||||
Db        342 GGGACACGACTG 353


RESULT 2
CB955875
LOCUS       CB955875                794 bp    mRNA    linear   EST 29-APR-2003
DEFINITION  AGENCOURT_13779371 NIH_MGC_184 Homo sapiens cDNA clone
            IMAGE:30349554 5', mRNA sequence.
ACCESSION   CB955875
VERSION     CB955875.1  GI:30211993
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 794)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM144  row: a  column: 19
            High quality sequence stop: 520.
FEATURES             Location/Qualifiers
     source          1. .794
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30349554"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_184"
                     /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
                     SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc);
                     Library is oligo-dT primed and directionally cloned. cDNA
                     was prepared from a glandular pool of tissues from thyoid,
                     parathyroid, adrenal, cortex and pineal gland.  5' and 3'
                     adaptors were used in cloning as follows: 5' adaptor
                     sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C, G, or T). Average insert size 1.38
                     kb (range 0.60-3.5 kb). 15/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match           74.1%;  Score 237.8;  DB 6;  Length 794;
  Best Local Similarity   83.8%;  Pred. No. 1.2e-65;
  Matches  269;  Conservative    0;  Mismatches   52;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         94 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 153

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||  |||||||| ||||||||||||||||||||||||||||||
Db        154 ATCACTTGCCGGGCAAGTCAGTACATTAGCACCTATTTAAATTGGTATCAGCAGAAACCA 213

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||  | || |||||     || | ||    |||   ||||||||
Db        214 GGGAAAGCCCCTAAATTACTGATTTATACTACAACCACTTTAGAACAGGGGGTCCCATCA 273

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||  ||||||| |||||||||| ||| ||||||||||||||| | ||||| | |
Db        274 AGGTTCACTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCCGTCTGCAACTT 333

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| | ||||||||||||||  | |||||||  ||| ||||||||||||||||
Db        334 GAAGATTTTGCAAATTACTTTTGTCAACAGAGTTACAGTTTCCCGGTCACCTTCGGCCAA 393

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||| ||| ||
Db        394 GGGACACGACTGGAGATTAAA 414


RESULT 3
BM171889
LOCUS       BM171889                621 bp    mRNA    linear   EST 04-DEC-2001
DEFINITION  imageqc_3_2001/smm27bdff41.x1 NIH_MGC_77 Homo sapiens cDNA clone
            IMAGE:4690877 5', mRNA sequence.
ACCESSION   BM171889
VERSION     BM171889.1  GI:17311452
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 621)
  AUTHORS   Kale,P.I., Harsch,T.J., Folta,P.A., Nelson,D.O., Sanders,C.G. and
            Prange,C.K.
  TITLE     The I.M.A.G.E. Consortium quality control effort: clone
            resequencing for verification
  JOURNAL   Unpublished (2001)
COMMENT     Other_ESTs: BG536784
            Contact: Prange CK
            The I.M.A.G.E. Consortium
            Lawrence Livermore National Laboratory
            Livermore, CA, USA
            Email: help@image.llnl.gov
            This read has been verified (found to hit its original self in the
            correct orientation), as part of the I.M.A.G.E. Consortium quality
            control effort. High quality sequence is defined as having 100 or
            more base pairs with a phred quality value of 20 or greater, where
            a sliding window of 4 base pairs with a phred quality value of 15
            or greater marks the beginning and end of the sequence. For
            information on obtaining this clone, please contact
            info@image.llnl.gov.
            Plate: LLCM1509  row: c  column: 6
            Seq primer: -21m13
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
     source          1. .621
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="IMAGE:4690877"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_77"
/note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1: SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.9 kb (range 0.5-4.0 kb). 12/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

```
  Query Match           73.6%;  Score 236.2;  DB 4;  Length 621;
  Best Local Similarity   83.5%;  Pred. No. 3.5e-65;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||   |||||||||||||||||||||||||||||| ||||||| ||||||||||||||||
Db         90 GATTGCCAGATGACCCAGTCTCCATCCTCCCTGTCTACATCTGTGGGAGACAGAGTCACC 149

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||| ||||| ||  |||||||||||||||| || ||||||
Db        150 GCCACTTGCCGGGCAAGTCAGAACATTAACAAATATTTAAATTGGTATCAACAAAAACCA 209

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              || ||  | |||||||| || |||||  | |||||  ||    | ||   ||||||||
Db        210 GGGCAAGCCCCTAAGCTCCTGATTTATGGTGCATCCACTTTGCAAAGTGGGGTCCCATCA 269

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||  |||||||  ||||||||||  |||  ||||||||||||||||||  ||||| |||
Db        270 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 329

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||||||| |||||||  |||||||| ||  || | | ||||||||||||||||||
Db        330 GAAGATTTTGCAACTTACTACTGTCAACAGACTTTCATTATCCCGATCACCTTCGGCCAA 389

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||| ||| ||
Db        390 GGGACACGACTGGAGATTAAA 410
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RESULT 4
CB957070
LOCUS CB957070 748 bp mRNA linear EST 29-APR-2003
DEFINITION AGENCOURT_13777897 NIH_MGC_184 Homo sapiens cDNA clone IMAGE:30350034 5', mRNA sequence.
ACCESSION CB957070
VERSION CB957070.1 GI:30213187
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 748)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
cDNA Library Preparation: CLONTECH Laboratories, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM145 row: e column: 19
High quality sequence stop: 507.
FEATURES Location/Qualifiers
source 1. .748

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30350034"
/lab_host="DH10B (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
/note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1: SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

```
  Query Match           73.6%;  Score 236.2;  DB 6;  Length 748;
  Best Local Similarity   83.5%;  Pred. No. 3.8e-65;
  Matches  268;  Conservative    0;  Mismatches   53;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||||||||||||||||||||||||||| | ||||||||||||||||
Db         89 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTATTGGAGACAGAGTCACC 148

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| ||| ||||||||||||||||||||||||||
Db        149 ATCACTTGCCGGGCAAGTCAGAGCATTACCAGTTATTTAAATTGGTATCAGCAGAAACCA 208

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  | ||  |||||  || || ||  ||     |||||       | ||   ||||||||
Db        209 GGGGAACCCCCTAACCTCCTGATCTATGCTGCATCCCGTTTGCAAAGTGGGGTCCCATCA 268

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||  |||||||  |||||  ||||  |||  |||||||||||||||||  ||||| |||
Db        269 AGGTTCAGTGGCAGTGGATCTGAGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 328

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              || ||||||||  ||||||||  |||||||||  | |||  |   ||||||||||||||||||
Db        329 GATGATTTTGCAACTTACTTCTGTCAACAGAGTTACAATACCCCGATCACCTTCGGCCAA 388

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||| ||| ||
Db        389 GGGACACGACTGGAGATTAAA 409
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RESULT 5
BG742662
LOCUS BG742662 826 bp mRNA linear EST 15-MAY-2001
DEFINITION 602633264F1 NCI_CGAP_Skn3 Homo sapiens cDNA clone IMAGE:4778726 5', mRNA sequence.
ACCESSION BG742662
VERSION BG742662.1 GI:14053315
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 826)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be

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            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10634 row: o column: 15
            High quality sequence stop: 824.
FEATURES              Location/Qualifiers
     source           1. .826
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:4778726"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NCI_CGAP_Skn3"
                      /note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;
                      Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                      Average insert size 1.5kb. Library constructed by Life
                      Technologies. Note: this is a NCI_CGAP Library."
ORIGIN

  Query Match            73.1%;  Score 234.6;  DB 4;  Length 826;
  Best Local Similarity  83.2%;  Pred. No. 1.3e-64;
  Matches  267;  Conservative    0;  Mismatches   54;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         55 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 114

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||||||||||||||||||||||| |||||||||||||| |||||||||| ||
Db        115 ATCACTTGCCGGGCAAGTCAGAGCATTAGCACCTATTTAAATTGGTTTCAGCAGAAATCA 174

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||| || || ||  |  | |||||  |  | | |    ||||||||
Db        175 GGGAAAGCCCCTAAACTCCTGATCCATGGTGCATCCAGTCTGCAGAGTGGGGTCCCATCA 234

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | ||||| ||||||| |||||||||| ||| |||||||||||||| || ||||| |||
Db        235 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGTAGTCTGCAACCT 294

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| | |||||  |||||||||  | |||||  | |||| ||||||||||||
Db        295 GAAGATTTTGCAATTTACTACTGTCAACAGGGTTACAGTCAGGCGATTACCTTCGGCCAA 354

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||| || ||| ||
Db        355 GGGACACGACTAGAGATTAAA 375


RESULT 6
CD690167
LOCUS       CD690167                709 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST6690 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD690167
VERSION     CD690167.1  GI:32210659
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 709)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES              Location/Qualifiers
     source           1. .709
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /tissue_type="normal nasopharynx"
                      /clone_lib="human nasopharynx"
                      /note="ESTs generated from a normal nasopharynx cDNA
                      library from southern Chinese"
ORIGIN

  Query Match            72.6%;  Score 233;  DB 6;  Length 709;
  Best Local Similarity  82.9%;  Pred. No. 4.1e-64;
  Matches  266;  Conservative    0;  Mismatches   55;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACC 182

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||| ||| |||||| |||||||| ||||||||||||||||||||||||||||
Db        183 ATCACTTGCCAGGCGAGTCAGGACATTAGCAACTATTTAAATTGGTATCAGCAGAAACCG 242

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||||| || || |||   ||||| |    ||||   ||||||||
Db        243 GGGAAAGCCCCTAAGCTCCTGATCTACGATGCATCCAATTTGGAAATAGGGGTCCCATCA 302

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
               | ||||| || |||| |||||||||| |||  ||| ||||||||||||||||||||||
Db        303 AGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCT 362

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||| |||| || || |  |||||||||| ||| | | | ||||||||||||||||
Db        363 GAAGATATTGCAACGTATTACTGTCAACAGTATGATAATCTCCGGATCACCTTCGGCCAA 422

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||| ||| ||
Db        423 GGGACACGACTGGAGATTAAA 443


RESULT 7
CB985512
LOCUS       CB985512                781 bp    mRNA    linear   EST 01-MAY-2003
DEFINITION  AGENCOURT_13672145 NIH_MGC_184 Homo sapiens cDNA clone
            IMAGE:30327573 5', mRNA sequence.
ACCESSION   CB985512
VERSION     CB985512.1  GI:30280036
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 781)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDCM136 row: m column: 22
            High quality sequence stop: 390.
FEATURES              Location/Qualifiers
     source           1. .781
                      /organism="Homo sapiens"
                      /mol_type="mRNA"
                      /db_xref="taxon:9606"
                      /clone="IMAGE:30327573"
                      /lab_host="DH10B (T1 phage-resistant)"
                      /clone_lib="NIH_MGC_184"
                      /note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
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SfiI (ggccattatggcc); Site_2: SfiI (ggccgcctcggcc); Library is oligo-dT primed and directionally cloned. cDNA was prepared from a glandular pool of tissues from thyoid, parathyroid, adrenal, cortex and pineal gland. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence: 5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A, C, or G and N = A, C, G, or T). Average insert size 1.38 kb (range 0.60-3.5 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 72.6%; Score 233; DB 6; Length 781;
Best Local Similarity 82.9%; Pred. No. 4.2e-64;
Matches 266; Conservative 0; Mismatches 55; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         89 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 148

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||||||||||||| || |||| ||||||||||||||||||| ||||| |||
Db        149 ATCACTTGTCGGGCAAGTCAGAGAATAAGCACCTATTTAAATTGGTATCAACAGAAGCCA 208

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||| || || || ||    ||||| |    | ||   ||||||||
Db        209 GGGAAAGCCCCTAACCTCCTAATCTATACTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 268

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| |||||||||||||||| ||||| |||
Db        269 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 328

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| ||||| |  |||||||||  | |||  |   |||  |||||||||||||
Db        329 GAAGATTTTGCCACTTATTACTGTCAACAGAGTTACAATACCCCGGTCACCTTCGGCCAA 388

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||||| ||
Db        389 GGGACACGACTGGACATTAAA 409
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RESULT 8
CD705041
LOCUS CD705041 553 bp mRNA linear EST 25-JUN-2003
DEFINITION EST21568 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD705041
VERSION CD705041.1 GI:32235671
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 553)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
source 1. .553
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 72.1%; Score 231.6; DB 6; Length 553;
Best Local Similarity 83.0%; Pred. No. 1.1e-63;
Matches 264; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        123 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCTTCTGTAGGAGACAGAGTCACC 182

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||    ||||||||||||||||||||||||||||
Db        183 ATCACTTGCCGGGCAAGTCAGAGCATTAGGTTCTATTTAAATTGGTATCAGCAGAAACCA 242

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||   |  | ||||| || || || ||    ||||| |    | ||   ||||||||
Db        243 GGGAAAGCCCCTAATCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATTA 302

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | | ||| ||||||| |||||||||| ||| |||||||||||||| ||| ||||| |||
Db        303 AGGTACAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCACCAGTCTGCAACCT 362

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||| || || |||  ||  |||| |||||||||
Db        363 GAAGATTTTGCAACTTACTACTGTCAACAGACTTACGGTTCCCCTCTCACTTTCGGCCAA 422

Qy        301 GGGACACGACTGGACATT 318
              ||||||||||||||| |||
Db        423 GGGACACGACTGGAGATT 440
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RESULT 9
AW406227
LOCUS AW406227 421 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BL0-acp-c-08-0-UI.r1 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3059726 5', mRNA sequence.
ACCESSION AW406227
VERSION AW406227.1 GI:6925284
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 421)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.
FEATURES Location/Qualifiers
source 1. .421
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3059726"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; Constructed from size fractionated cytoplasmic mRNA

(1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 72.1%; Score 231.4; DB 2; Length 421;
Best Local Similarity 82.6%; Pred. No. 1.1e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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              ||  |||||||||||||||||||||| ||| ||||||||||||||||||||| |||||||
Db         10 GACATCCAGATGACCCAGTCTCCATCTTCCGTGTCTGCATCTGTAGGAGACACAGTCACC 69

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||| |  || ||||||  |||   ||||||||||||||||||
Db         70 ATCACTTGTCGGGCGAGTCAGGGTCTTGGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA 129

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||      | ||||||||  ||  | ||     ||||| |     | ||   ||||||||
Db        130 GGGACTGCCCCTAAGCTCCTGCTCTATGCTGCATCCAATTTGCAAAGTGGGGTCCCATCA 189

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||||||||||| |||||||||| ||| ||||||||||||  ||||||||||||
Db        190 AGGTTCAGCGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCGACAGCCTGCAGCCT 249

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||||||||||| |||||||||| || ||| ||| ||||||||||||||||||
Db        250 GAAGATTTTGCTACTTACTATTGTCAACAGGCTAACACTTTCCCGATCACCTTCGGCCAA 309

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||||||| ||
Db        310 GGGACACGACTGGACATTAAA 330
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RESULT 10
AW407904
LOCUS AW407904 422 bp mRNA linear EST 16-FEB-2000
DEFINITION UI-HF-BL0-add-a-01-0-UI.r2 NIH_MGC_37 Homo sapiens cDNA clone IMAGE:3061128 5', mRNA sequence.
ACCESSION AW407904
VERSION AW407904.1 GI:6926961
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 422)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Seq primer: M13 Forward.

FEATURES Location/Qualifiers
source 1. .422
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3061128"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
/lab_host="DH10B (LTI)"
/clone_lib="NIH_MGC_37"
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA (1.5-2.5kb). Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 72.1%; Score 231.4; DB 2; Length 422;
Best Local Similarity 82.6%; Pred. No. 1.1e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         23 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 82

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         83 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 142

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||||  || || ||     ||||| |     | ||   ||||||||
Db        143 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 202

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||||| ||||| |||
Db        203 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 262

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||||  |||||||  |||||||||  | |||||   |||   || |||||||||
Db        263 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCGTGGACGTTCGGCCAA 322

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||      |||| ||  ||
Db        323 GGGACCAAGGTGGAAATCAAA 343
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RESULT 11
CD707755
LOCUS CD707755 521 bp mRNA linear EST 25-JUN-2003
DEFINITION EST24282 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD707755
VERSION CD707755.1 GI:32238385
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 521)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.

FEATURES Location/Qualifiers
source 1. .521
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"

ORIGIN

Query Match 72.1%; Score 231.4; DB 6; Length 521;
Best Local Similarity 82.6%; Pred. No. 1.2e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         91 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 150

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||| ||| ||||||  ||| | |  ||||||||||||||||||||||||||||
Db        151 ATCACTTGCCAGGCGAGTCAGGACATAAACTACTATTTAAATTGGTATCAGCAGAAACCA 210

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | ||||||| || || |||   ||||| |    |||| | ||||||  |
Db        211 GGGAAAGCCCCTAAGCTCCTGATCTACGATGCATCCATTTTGGAAACAGGGGTCTCATCA 270

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| || |||| |||||||||| |||  ||| ||||||||| ||||||||||||
Db        271 AGGTTCAGTGGAAGTGGATCTGGGACAGATTTTACTTTCACCATCACCAGCCTGCAGCCT 330

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||  |||| || || |  |||||||||| ||| | | | ||||||||||||||||
Db        331 GAAGATATTGCAACATATTACTGTCAACAGTTTGATAATCTCCCGATCACCTTCGGCCAA 390

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        391 GGGACACGACTGGAGATTAAA 411
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RESULT 12
BG756289
LOCUS BG756289 587 bp mRNA linear EST 15-MAY-2001
DEFINITION 602713607F1 NIH_MGC_48 Homo sapiens cDNA clone IMAGE:4853953 5', mRNA sequence.
ACCESSION BG756289
VERSION BG756289.1 GI:14066942
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 587)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1700 row: n column: 02
High quality sequence stop: 586.
FEATURES Location/Qualifiers
source 1. .587
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4853953"
/tissue_type="primary B-cells from tonsils (cell line)"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_48"
/note="Organ: B-cells; Vector: pOTB7; Site_1: XhoI; Site_2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library."
ORIGIN

Query Match 72.1%; Score 231.4; DB 4; Length 587;
Best Local Similarity 82.6%; Pred. No. 1.3e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTGGGAGACAGAGTCACC 136

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||||| ||| ||||||   |||||  ||||||||||||||||||||||||||||
Db        137 ATCACTTGCCAGGCGAGTCAGGATATTAGTTACTATTTAAATTGGTATCAGCAGAAACCA 196

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||| |  | ||||||| || || |||   ||||| |    ||||   ||||||||
Db        197 GGAAAAGCCCCTAAGCTCCTGATCTACGATGCATCCAATTTGGAAATAGGGGTCCCATCA 256

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||  ||| |||||||||| |||  ||| ||||||||||||||||||||||
Db        257 AGGTTCAGTGGGCGTGGATCTGGGACAGATTTTACTTTCACCATCAGCAGCCTGCAGCCT 316

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              ||||||  |||| || || |  |||||||| |  ||| ||| | ||||||||||||||||
Db        317 GAAGATATTGCAACATATTATTGTCAACGGCATGATAGTCTCCCGATCACCTTCGGCCAA 376

Qy        301 GGGACACGACTGGACATTCAA 321
              ||||||||||||||| ||| ||
Db        377 GGGACACGACTGGAAATTAAA 397
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RESULT 13
CD690145
LOCUS CD690145 624 bp mRNA linear EST 25-JUN-2003
DEFINITION EST6668 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION CD690145
VERSION CD690145.1 GI:32210615
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 624)
AUTHORS Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and Zeng,Y.-X.
TITLE Transcriptional Gene Expression Profile of Human Nasopharynx
JOURNAL Unpublished (2003)
COMMENT Contact: YiXin Zeng
Cancer Center
Sun Yat-sen University
651 DongFeng Road East, GuangZhou 510060, China
Tel: 86-1380-9770-743
Fax: 86-20-8775-4506
Email: yxzeng@gzsums.edu.cn.
FEATURES Location/Qualifiers
source 1. .624
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/tissue_type="normal nasopharynx"
/clone_lib="human nasopharynx"
/note="ESTs generated from a normal nasopharynx cDNA library from southern Chinese"
ORIGIN

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Best Local Similarity 82.6%; Pred. No. 1.3e-63;
Matches 265; Conservative 0; Mismatches 56; Indels 0; Gaps 0;

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Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Db        114 GACATCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 173

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        174 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 233
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Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
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Db        234 GGGAAAGCCCCTAAGCTCCTGATCTATGCTGCATCCAGTTTGCAAAGTGGGGTCCCATCA 293

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
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Db        294 AGATTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 353

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||| | |||||   || |  || || |||||
Db        354 GAAGATTTTGCAACTTACTACTGTCAACAGAGTTACAGTACCCCTAGAACTTTTGGCCAG 413

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||    ||||| ||  ||
Db        414 GGGACCAAGCTGGAGATCAAA 434


RESULT 14
BG536784
LOCUS       BG536784                 570 bp    mRNA    linear   EST 03-APR-2001
DEFINITION  602566318F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4690877 5',
            mRNA sequence.
ACCESSION   BG536784
VERSION     BG536784.1  GI:13528330
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 570)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: CLONTECH Laboratories, Inc.
             cDNA Library Preparation: CLONTECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1509  row: c  column: 06
            High quality sequence stop: 568.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_77"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc); 5' and
                     3' adaptors were used in cloning as follows: 5' adaptor
                     sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor sequence:
                     5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3' (where B = A,
                     C, or G and N = A, C,  G, or T).  Average insert size 1.9
                     kb (range 0.5-4.0 kb). 12/15 colonies contained inserts
                     by PCR. This library was enriched for full-length clones
                     and was constructed by Clontech  Laboratories (Palo Alto,
                     CA). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             71.8%;  Score 230.6;  DB 4;  Length 570;
  Best Local Similarity   84.4%;  Pred. No. 2.3e-63;
  Matches  271;  Conservative    0;  Mismatches   49;  Indels    1;  Gaps    1;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
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Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              ||||||||||||||||||||||| ||||| ||  |||||||||||||||| || ||||||
Db        151 GTCACTTGCCGGGCAAGTCAGAACATTAACAAATATTTAAATTGGTATCAACAAAAACCA 210

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |||| |||||||| || |||||  | |||||  ||    | ||   ||||||||
Db        211 GGCAAGCC-CCTAAGCTCCTGATTTATGGTGCATCCACTTTGCAAAGTGGGGTCCCATCA 269

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | ||||| ||||||| |||||||||| ||| ||||||||||||||||| ||||| |||
Db        270 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT 329

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
              |||||||||| |||||||  |||||||| ||  || | | ||||||||||||||||||
Db        330 GAAGATTTTGCAACTTACTACTGTCAACAGACTTTCATTATCCCGATCACCTTCGGCCAA 389

Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||| ||| ||
Db        390 GGGACACGACTGGAGATTAAA 410


RESULT 15
CD683960
LOCUS       CD683960                 486 bp    mRNA    linear   EST 25-JUN-2003
DEFINITION  EST480 human nasopharynx Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD683960
VERSION     CD683960.1  GI:32198500
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 486)
  AUTHORS   Liu,X.-Q., Zhou,Y., Zhang,L.-J., Xu,H., Chen,H.-K., Pan,Z.-G. and
            Zeng,Y.-X.
  TITLE     Transcriptional Gene Expression Profile of Human Nasopharynx
  JOURNAL   Unpublished (2003)
COMMENT     Contact: YiXin Zeng
            Cancer Center
            Sun Yat-sen University
            651 DongFeng Road East, GuangZhou 510060, China
            Tel: 86-1380-9770-743
            Fax: 86-20-8775-4506
            Email: yxzeng@gzsums.edu.cn.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="normal nasopharynx"
                     /clone_lib="human nasopharynx"
                     /note="ESTs generated from a normal nasopharynx cDNA
                     library from southern Chinese"
ORIGIN

  Query Match             71.6%;  Score 229.8;  DB 6;  Length 486;
  Best Local Similarity   82.2%;  Pred. No. 3.9e-63;
  Matches  264;  Conservative    0;  Mismatches   57;  Indels    0;  Gaps    0;

Qy          1 GAGCTCCAGATGACCCAGTCTCCATCCTCCCTGTCTGCATCTGTAGGAGACAGAGTCACC 60
              ||  |||||||||||||| |||||| ||| ||||||||||||||||||||||||||||
Db        134 GACATCCAGATGACCCAGTTTCCATCTTCCGTGTCTGCATCTGTAGGAGACAGAGTCACC 193

Qy         61 ATCACTTGCCGGGCAAGTCAGAGCATTAGCAGCTATTTAAATTGGTATCAGCAGAAACCA 120
              |||||||| ||||| |||||||  ||||||||||  |||  ||||||||||||||||||
Db        194 ATCACTTGTCGGGCGAGTCAGGATATTAGCAGCTGGTTAGCCTGGTATCAGCAGAAACCA 253

Qy        121 GGACAGCCTCCTAAGCTGCTCATTTACTGGGCATCTACCCGGGAATCCGGGGTCCCTGAC 180
              ||  |  | |||||| | || || ||    ||||| |       ||   ||||||||
Db        254 GGGAAAGCCCCTAAGGTCCTGATCTATGCTGCATCCAATTTACAAAGTGGGGTCCCATCA 313

Qy        181 CGATTCAGCGGCAGTGAATCTGGGACAAATTACACTCTCACCATCAGCAGCCTGCAGCCT 240
              | |||||||||||||| |||||||||||.| ||||||||||||||||||||||||||||
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Db        314 AGGTTCAGCGGCAGTGGATCTGGGACAAAATTCACTCTCACCATCAGCAGCCTGCAGCCT 373

Qy        241 GAAGATTTTGCTACTTACTTTTGTCAACAGTCTGACAGTTTGCCGATCACCTTCGGCCAA 300
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Qy        301 GGGACACGACTGGACATTCAA 321
              |||||||||||||| ||| ||
Db        434 GGGACACGACTGGAGATTAAA 454
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Search completed: December 7, 2004, 11:13:52
Job time : 1875.31 secs

BACKFILE DOCUMENT INDEX SHEET

A DOCPHOENIX

APPL PARTS

IMIS
Internal Misc. Paper
LET
Misc. Incoming Letter

371P
PCT Papers in a 371Application

A...
Amendment Including Elections

ABST
Abstract

ADS
Application Data Sheet

AF/D
Affidavit or Exhibit Received

APPENDIX
Appendix

ARTIFACT
Artifact

BIB
Bib Data Sheet

CLM
Claim

COMPUTER
Computer Program Listing

CRFL
All CRF Papers for Backfile

DIST
Terminal Disclaimer Filed

DRW
Drawings

FOR
Foreign Reference

FRPR
Foreign Priority Papers

IDS
IDS Including 1449

NPL
Non-Patent Literature

OATH
Oath or Declaration

PET.
Petition

RETMAIL
Mail Returned by USPS

SEQLIST
Sequence Listing

SPEC
Specification

SPEC NO
Specification Not In English

TRNA
Transmittal New Application

OUTGOING

CTMS
Misc. Office Action

1449
Signed 1449

892
892

ABN
Abandonment

APDEC
Board of Appeals Decision

APEA
Examiner Answer

CTAV
Count Advisory Action

CTEQ
Count Ex parte Quayle

CTFR
Count Final Rejection

CTNF
Count Non-Final

CTRS
Count Restriction

EXIN
Examiner Interview

M903
DO/EO Acceptance

M905
DO/EO Missing Requirement

NFDR
Formal Drawing Required

NOA
Notice of Allowance

PETDEC
Petition Decision

INCOMING

AP.B
Appeal Brief

C.AD
Change of Address

N/AP
Notice of Appeal

PA..
Change in Power of Attorney

REM
Applicant Remarks in Amendment

XT/
Extension of Time filed separate

Internal

SRNT
Examiner Search Notes

CLMPTO
PTO Prepared Complete Claim Set

ECBOX
Evidence Copy Box Identification

WCLM
Claim Worksheet

WFEE
Fee Worksheet

File Wrapper

FWCLM
File Wrapper Claim

IIFW
File Wrapper Issue Information

SRFW
File Wrapper Search Info